

GenCore version 5.1.4.P5.4578
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OM nucleic - nucleic search, using sw model

Run on: March 18, 2003, 06:43:25 ; Search time 3256 Seconds

(without alignments)
10627.529 Million cell updates/sec

Title: US-09-857-613A-27

Perfect score: 1189
Sequence: 1 ggcacatggccacccgtgtgtg.....aaaaaaaaaaaaaaaaaaaaa 1189

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenBank:*

- 1: gb_ba:*
- 2: gb_hlg:*
- 3: gb_in:*
- 4: gb_ov:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pt:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_un:*
- 15: gb_vl:*
- 16: em_ba:*
- 17: em_fun:*
- 18: em_hum:*
- 19: em_mu:*
- 20: em_om:*
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- 22: em_ov:*
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- 32: em_hlg_other:*
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- 35: em_hlg_rtd:*
- 36: em_hlg_mam:*
- 37: em_hlg_vrt:*
- 38: em_sy:*
- 39: em_higo_hum:*
- 40: em_higo_mus:*
- 41: em_higo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|------------|--------------------|
| 1 | 456.8 | 38.4 | 1369 | 8 AF213481 | AF213481 Perilla f |
| 2 | 445.2 | 37.4 | 1303 | 8 AY049258 | AY049258 Arabidops |
| 3 | 443.6 | 37.3 | 1047 | 8 AY090280 | AY090280 Arabidops |
| 4 | 442 | 37.2 | 1350 | 6 AX417728 | AX417728 Sequence |
| 5 | 440.4 | 37.0 | 1296 | 8 AF104220 | AF104220 Arabidops |
| 6 | 440.4 | 37.0 | 1296 | 8 AY087138 | AY087138 Arabidops |
| 7 | 192.2 | 16.2 | 118335 | 8 AC006193 | AC006193 Arabidops |
| 8 | 149.4 | 12.6 | 343550 | 1 AP003587 | AP003587 Nostoc sp |
| 9 | 147 | 12.4 | 134199 | 1 SYCSTRF | D64004 Synechocyst |
| 10 | 110 | 9.3 | 125422 | 2 AF003994 | AF003994 Oryza sat |
| 11 | 99.4 | 8.4 | 108553 | 8 AF527809 | AF527809 Sorghum b |
| 12 | 76.6 | 6.4 | 930 | 6 AX073663 | AX073663 Sequence |
| 13 | 76.6 | 6.4 | 957 | 6 AX073657 | AX073657 Sequence |
| 14 | 76.6 | 6.4 | 957 | 6 AX417730 | AX417730 Sequence |
| 15 | 76.6 | 6.4 | 974 | 6 AX073659 | AX073659 Sequence |
| 16 | 76.6 | 6.4 | 145709 | 1 D90914 | D90914 Synechocyst |
| 17 | 68.8 | 5.8 | 334520 | 1 AP003588 | AP003588 Nostoc sp |
| 18 | 67.4 | 5.7 | 298750 | 1 AP005375 | AP005375 Thermosyn |
| 19 | 51.6 | 4.3 | 218856 | 2 AC009282 | AC009282 Rattus no |
| 20 | 51 | 4.3 | 7218 | 6 166494 | 166494 Sequence 14 |
| 21 | 50.6 | 4.3 | 293545 | 2 AC008276 | AC008276 Rattus no |
| 22 | 50 | 4.2 | 10969 | 8 SPAC19E9 | Z98975 S.pombe chr |
| 23 | 49 | 4.1 | 1665 | 3 AB025584 | AB025584 Dictyoste |
| 24 | 49 | 4.1 | 234488 | 2 AC109698 | AC109698 Rattus no |
| 25 | 48.4 | 4.1 | 1851 | 9 AB064996 | AB064996 Macaca fa |
| 26 | 48.2 | 4.1 | 25681 | 1 SAE41559 | AJ414559 Saccharot |
| 27 | 48.2 | 4.1 | 32070 | 2 AC116983 | AC116983 Dictyoste |
| 28 | 48 | 4.0 | 67970 | 3 PFMA1IP3 | AI031746 Plasmodiu |
| 29 | 48 | 4.0 | 180260 | 2 AC107168 | AC107168 Rattus no |
| 30 | 47.8 | 4.0 | 1410 | 6 E07846 | AC107168 Rattus no |
| 31 | 47.8 | 4.0 | 5998 | 1 AB032524 | E07846 DNA sequenc |
| 32 | 47.8 | 4.0 | 7143 | 6 AX345885 | AB032524 Streptomy |
| 33 | 47.6 | 4.0 | 161557 | 2 AC009826 | AX345885 Sequence |
| 34 | 47.6 | 4.0 | 193024 | 2 AC073855 | AC009826 Homo sapi |
| 35 | 47.6 | 4.0 | 107289 | 2 AC079859 | AC073855 Homo sapi |
| 36 | 47.2 | 4.0 | 206214 | 2 AC116923 | AC079859 Homo sapi |
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| 38 | 46.8 | 3.9 | 128124 | 2 AC113915 | AX006889 Sequence |
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| 40 | 46.6 | 3.9 | 2180 | 8 AB028665 | AX344572 Sequence |
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| 42 | 46.4 | 3.9 | 298406 | 3 CEY7588A | AC096310 Rattus no |
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| 44 | 46.2 | 3.9 | 154611 | 2 AC068893 | AC116306 Dictyoste |
| 45 | 46.2 | 3.9 | 170742 | 2 AC109078 | AC068893 Homo sapi |

ALIGNMENTS

RESULT 1
LOCUS AF213481 1369 bp mRNA linear PLN 02-DEC-200
DEFINITION Perilla frutescens gamma-tocopherol methyltransferase (TMT) mRNA,
complete cds.
ACCESSION AF213481
VERSION AF213481
KEYWORDS
SOURCE
ORGANISM
Perilla frutescens
Perilla frutescens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; eusterids I; Lamiales; Lamiales; Asteraceae; Perilla.
REFERENCE
1 (bases 1 to 1369)
Kim, K.-H., Hwang, S.-K. and Hwang, Y.-S.

| TITLE | JOURNAL | REFERENCE | AUTHORS | TITLE | JOURNAL | FEATURES |
|--------------------------------------------------------------|--------------------------------------------------------------------|--------------------------------------------------------|---------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------|------------------------------------------------------|
| Cloning of <i>Perilla</i> gamma-tocopherol methyltransferase | Unpublished | 2 (bases 1 to 1369) | Kim, K.-H., Hwang, S.-K. and Hwang, Y.-S. | Submitted (09-DEC-1999) Division of Biochemistry, National Institute of Agricultural Science and Technology, 249 Seodun-dong, Kwonson-gu, Suwon, Kyunggi-do 441-707, Republic of Korea | Location/Qualifiers | 1. .1369 |
| gene | CDS | /organism="Perilla frutescens" | /cultivar="Okdong" | /db_xref="taxon:48386" | /rissue_type="developing seed" | 1. .1369 |
| | | /gene="TMT" | 89. .1198 | /gene="TMT" | /codon_start=1 | /product="gamma-tocopherol methyltransferase" |
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| | | YLARKYGAKLSRAITFLSSPVQAOARQADADQNGKVSFEVADALNDPFEQFDIV | WSMEGHEMPDKRFFVNEIVRAVAGGRIILVTYCHNRDLSSESLRQREEDLINKIT | SAYILPAMCTADYVKILKLDLSMEDIKADMSHDVAPFPWPAIVISALTWKQITSLNS | GKMTIRGAMVNPIMIEGKKKVIKFIATITCKRPAS" | |
| BASE COUNT | 380 a | 306 c | 332 g | 351 t | | |
| ORIGIN | | | | | | |
| Query Match | 38.4% | Score 456.8: | DB 8: | Length 1369; | | |
| Best Local Similarity | 71.2% | Pred. No. 3.4e-105; | | | | |
| Matches 634: | Conservative | 0; | Mismatches 247; | Indels 9; | Gaps 2; | |
| 115 | CAAGAAGATGACAAAGAACAGCTGCAGAGGGAATCGACAGATTTCAGACGATCGTC | 234 | | | | |
| Db | 304 GATGGAGACGGAGATGAGAGACCTTCGTAAGAGGATTCGGAGTTCFAGAGAGATCGTC | 363 | | | | |
| QY | 235 TGGCTTATGGGAGAACATTTGGGGGACACATGACCATGAGCTTTTATGACTCGGATTC | 294 | | | | |
| Db | 364 GGGGATGTGGAGAACATATGGGGAGACCATGACACGCGCTTTACGAGCGCGCGC | 423 | | | | |
| QY | 295 CACTCTTTCGCTTCGATGATCACTGCTGCTCAGATTCGGAATGATCCAAGATCTCTTCG | 354 | | | | |
| Db | 424 CGAGCTTCACATCTCGACACATCGCGCGCCGACAGATCCGATGATGAGAGTCCCTCG | 483 | | | | |
| QY | 355 CTTTCCCTCTGTTTGTGAGAGAGCTAGTA---AATGCCAAGAGATATGTTGATGTTGG | 411 | | | | |
| Db | 484 ATTCCCTCTCTCTCCGATTAACATACAGCAGAGAACCCAGAAATATATGTTGATGTGG | 543 | | | | |
| QY | 412 GTGTGCATAGGTGGCAGCTCTAGTACCCTGGCCCAAGAAATTTGGAGCA-----CCAG | 465 | | | | |
| Db | 544 ATGTGCTATAGAGGCACTTCTAGGTATCTGGCAAGAAATATGCGGCTAAATTTGCTAG | 603 | | | | |
| QY | 466 TGTAGGCATCACTCGATCTCTGTTCAAGCTCAAGAACCAATGCTCTGCTGGCGTCA | 525 | | | | |
| Db | 604 GGCATTAATCTCTCCACACCCCTGTGCAAGCCAGAGAGCTTAACAGCTTGTGTAGTCTCA | 663 | | | | |
| QY | 526 AGGATTTGCTCATTAAGGTTTCTTTCAAGTTGCTGACGCTCTACAGCAACCATCTCTGTA | 585 | | | | |
| Db | 664 AGGATTAATATGCAAGGTTTCTTTGAAGTTGCTGATGCGTTGAACCAACCATTTCTGTA | 723 | | | | |
| QY | 586 CGGCGCATTTGATCTGGTGTGTGCTCATAGAGAGATGAGAGCATATGCTCTGACAAAGCTAA | 645 | | | | |
| Db | 724 AGGGAAGTTGATCTGTGTTGGTGTGATGAGAGAGTGGAGAACACATGCTGATAGAAATA | 783 | | | | |
| QY | 646 GTTTGTTGAGAGATTACCTCGGATGAGAGACCAAGGCGCATTAATATATATAGTAACATG | 705 | | | | |
| Db | 784 GTTTGTAATATGAGCTGTGCTGTGCTGCTCTCTGTTGGAGAAAGATATATATCTGTTACATG | 843 | | | | |
| QY | 706 GTGCCACAGGAGATTTGGCCCTGACGAACATCTTTCATCTCATATGGAGCAAGATCTCTT | 765 | | | | |

| | | | | |
|------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------|-----------------------------------------------------------|--------|
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| OY | 766 | AAGAAGATTTCGGATGCATATTACTCCTCGCTGGTGCTCAACTTCGATTAATTTGA | 825 | |
| Df | 904 | AAAACAAATATGTAGTCTTATATCTTCAGCATGTGTGCTTACTGTGACATATGCA | 963 | |
| OY | 826 | GTTGTCATATCCCTGTCACCTTAGACACATCAAGTCAGAAAGATGGTCTGCTTTGGC | 885 | |
| Df | 964 | ATTACTGACTCCCTCTCATATGAGACATAAAGTGTGACAGTGGTGTGACCATTGCG | 1023 | |
| OY | 886 | TCCATTTTGGCCAGCATGATACGCTCACGCTTCACATGGAAGGGCTATCTTCACTCTT | 945 | |
| Df | 1024 | TCCATTTTGGCCGAGATTATAAAGTCGGCATTTGACATGGAAGGCATTAACCTCATGCT | 1083 | |
| OY | 946 | GAGCAGTGCACAAAAAACGATAAAGAGACCTTTGGCTATGCCATTGATGATAGAGGATA | 1005 | |
| Df | 1084 | AAGGACGGATGATGAMACATTAAGAGACGAACATGATGATGATGATGATGATGATGATG | 1143 | |
| OY | 1006 | CAGAAGAAGTCAATTAATTAAGTTGGCATCTATTCATCATGTCGAAAAACCTGAT | 1055 | |
| Df | 1144 | TAGAAGGCGCTGATCAAAATTTGCCATTCATCATGTCGAAAAACCTGAT | 1193 | |
| RESULT 2 | | | | |
| LOCUS | AY049258 | 1303 bp | mRNA | linear |
| DEFINITION | Arabidopsis thaliana Atlg64970/Ft13011_27 mRNA, complete cds. | | | |
| ACCESSION | AY049258 | | | |
| VERSION | AY049258.1 | GI:15146233 | | |
| KEYWORDS | PLI CDNA. | | | |
| SOURCE | Arabidopsis thaliana | | | |
| ORGANISM | Arabidopsis thaliana | | | |
| REFERENCE | 1 (bases 1 to 1303) | | | |
| AUTHORS | Chewk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J., Bower L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S., Shinzaki K., Davis R.W., Theologis A. and Eckert J.R. | | | |
| TITLE | Arabidopsis cDNA clones | | | |
| JOURNAL | Unpublished | | | |
| REFERENCE | 2 (bases 1 to 1303) | | | |
| AUTHORS | Chewk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J., Bower L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S., Shinzaki K., Davis R.W., Theologis A. and Eckert J.R. | | | |
| TITLE | Direct Submission | | | |
| JOURNAL | Submitted (22-JUL-2001) Salk Institute Genomic Analysis Laboratory (Stigall), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA | | | |
| COMMENT | RKEN Genomic Sciences Center (GSC) members carried out the sequencing and annotation of the RAFL cDNAs (RAFL cDNA : 'RKEN Arabidopsis Full-length cDNA') : Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinzaki,K. | | | |
| | The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Chewk R., Chen H., Kim,C.J., Koesema,E., Meyers,M.C., Shinn,P., Banh,J., Bower,L., Dale,J.M., Goldsmith,A.D., Jiang,P.X., Jones,T., Kamiya,A., Karlin-Neumann,G., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Nguyen,M., Onodera,C.S., Palm,C.J., Pham,P.K., Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C., Toriumi,M., Yamada,K., Yamamura,Y., Yu,G., Yu,S., Shinzaki,K., Davis,R.W., Theologis,A. and Eckert,J.R. | | | |

Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Davis, R.W., Theologis, A., and Becker, J.R.

Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Becker, J.R. (SSP/Salk) contributed equally to this work as PIs.

FEATURES

Location/Qualifiers

1. 1303

/organism="Arabidopsis thaliana"

/db_xref="taxon:3702"

/chromosome="1"

/clone="RAF107-18-C14(R13225)"

/note="ecotype: Columbia"

1. 67

5. 1114

/note="gamma-tocopherol methyltransferase"

/codon_start=1

/product="At1g64970/F13011_27"

/protein_id="AAK83600.1"

/db_xref="GI:15146234"

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5'UTR

68. 1114

3'UTR

1115. 1303

BASE COUNT

352 a 267 c 307 g 377 t

ORIGIN

Query Match 37.4% Score 445.2 DB: 8 Length 1303;
Best Local Similarity 70.5% Pred. No. 3e-102;
Matches 626; Conservative 0; Mismatches 253; Indels 9; Gaps 2;

187 CAAGAAGAGCTGCAGAGGAGGAGTGCAGAGCTTTACGACGAGTGTGCTTATGGA 246
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295 AGAGATTGGGAGATCATATGCTATGCTTTTATGACCTGATCTTCTGTTCAACT 354
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718 TCTTGGCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 777
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Db 775 TCTATCTGGGGGAGAGAGAGCTTTGACGCCGTGGGAGCAAAACATTTGGACAAATCTG 834
Qy 778 CGATGATATTAACCTCCCTGCGTGCCTCAACTTGTATATTAAGTTCCTCCATC 837
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Db 835 TAAGAGCTTCTATCTCCGCTTGGCTGCTCCACAGATATGATGATGATGATGAT 894
Qy 838 CCTGTCACCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 897
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Db 895 CCATTCCTCCAGAGATATTAAGTTCGCGATGTCGAGAGAGAGAGAGAGAGAGAG 954
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Db 1075 CATTAAGTTTGGTATCATCATCTGCGAGAGAGAGAGAGAGAGAGAGAG 1122

RESULT 3
AY090280 1047 bp mRNA linear PLN 24-MAR-2002
LOCUS Arabidopsis thaliana At1g64970/F13011_27 mRNA, complete cds.
DEFINITION
ACCESSION AY090280
VERSION AY090280.1 GI:19699149
KEYWORDS
SOURCE FLI_CDNA.
ORGANISM Arabidopsis thaliana.
Arabidopsis thaliana.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1047)
REFERENCE
AUTHORS Kim, C.J., Chen, H., Cheuk, R., Meyers, M.C., Shinn, P., Banh, J.,
Bowser, L., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D.,
Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G.,
Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M.,
Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T.,
Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C.,
Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W.,
Theologis, A., and Becker, J.R.
TITLE Arabidopsis ORF clones
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1047)

TITLE
JOURNAL
COMMENT
USA
RIKEN Genomic Sciences Center (GSC) members carried out the
sequencing and annotation of the RFLF cDNAs (RAF1 cDNA, 'RIKEN
Arabidopsis Full-Length cDNA'), Seki, M., Narusaka, M., Ishida, J.,
Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,
Hayashizaki, Y., and Shinozaki, K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the
sequencing and annotation of the RFLF cDNAs: Kim, C.J., Chen, H.,
Cheuk, R., Meyers, M.C., Shinn, P., Banh, J., Bowser, L., Chang, E.,
Dale, J.M., Goldsmith, A.D., Jones, T., Karlin-Neumann, G., Lam, B.,
Lee, J.M., Lin, J., Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J.,
Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C.,
Yamada, K., Yamamura, Y., Yu, G., Yu, S., Davis, R.W., Theologis, A.,

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| | QARKNAALAAASLSLHKSAPVDALDOPFEDGKFDLWMSMESGFMHDKRKFVEL | | |
| | RVAAPGRRIITITVMCHRLSLSGEALDQPMENILDKICKTYFLAMGSTDDIVNLKQ | | |
| | HSIDLIKADMSENVAPFPVAVIRATLTKVLISLRBGMKSIKALITMPIMIBEYK | | |
| | GVIFGIITCKPKP" | | |
| BASE COUNT | 374 a | 278 c | 314 g 384 t |
| Query Match | 37.2% | Score 442; | DB 8; Length 1350; |
| Best Local Similarity | 70.3% | Pred. No. 1.9e-101; | |
| Matches 624; | Conservative 0; | Mismatches 255; | Indels 9; Gaps 2 |
| QY | 187 CAAGAAGAAGCGGCAAGGAGGACAGATTTTACGACGAGTGTGCTGGCTATAGGA | 246 | |
| DB | 230 CACTGAGCGCGCTAAAGAAAGAAATACGGAGTCTTCAATGAACCTCGGGTTTGCGGA | 289 | |
| QY | 247 GAAACATTTGGGGCGACCAACATCCACCATGGCTTTTATAGTCGGATTCACGTGTCGT | 306 | |
| DB | 290 AGAGATTTGGGGAGATCATATGCAATCATCGCTTTTATGACCCGTATTCCTTGTCACAT | 349 | |
| QY | 307 TTGCGATCATCGT-----GCTGCTCAGATCCGATGATCCAAAGATCTCTTCGCTTTC | 360 | |
| DB | 350 TTCTCATTTCTGGCTCAACAAAGAGCGATCGATCCGTATGATGAAGAGCTCTCCGTTTCC | 409 | |
| QY | 361 CTCCTGTTTC---TGAAGACCGTATTAATAGGCCCAAGACGATATPAGATGTTGGGCTGG | 417 | |
| DB | 410 CGCTTTACTATGATGAGAGAGAGAGAGAAAAAGATTAAGAAAGTATGATGATTTGGCTGG | 469 | |
| QY | 418 CATAGGTGACGCTCTAGATACCTGGCCCAAGAAATTTGGAGCAACGATGTAGCAATCAC | 477 | |
| DB | 470 GATTGGAGGAACTCAAGATATCTTCCCTCTAAATTTGGAGCGATGATGATTTGGCAATTA | 529 | |
| QY | 478 TCTGATGCTCTGTTCAAGCTCAAGAGCAAAATGCTCTTGGCTGCTCTCAAGATTTGGCTGA | 537 | |
| DB | 530 TCTCAGCCCTGTTCAAGGCCAAGAGCAACCAATGATCTCGCGGCTCAATCACTCTCTCA | 589 | |
| QY | 538 TAAGGTTTCCCTTCAGTGTGCTGAGGCTCTGACAGCAACCTCTCTGACGGCCAGTTTGA | 597 | |
| DB | 590 TAAGGCTTCCCTTCCAAAGTTGGCGGATCGTTGGATACCAATTTGAAAGATGAAAAATTTCCA | 649 | |
| QY | 598 TCTGGTGTGCTCATATGAGAGTGAAGCATATGACCTGACCAAGACTAAAGTTTGTGGAGA | 657 | |
| DB | 650 TCTAGTGTGTGATGATGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG | 709 | |
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| QY | 718 TCTTGGCCCTGACAGCAACATCTTACATATCCATGGGAGCAAGATCTCTTAAAGAAATTTG | 777 | |
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| DB | 830 TAAGACGTTCTATCTCCCGCTTGTGTCTCCACCGATATATATATATATATATATATATAT | 889 | |
| QY | 838 CCTGTCATTTCAAGACATCAAGTCAGAAATGCTGCTCGCTTGTGTCTCCATTTTGGCC | 897 | |
| DB | 890 CCATCTCTCCACAGATATTAAGTGTGGAGATGTGTCAGAAAGATGACTCTCTTCTGCGCC | 949 | |
| QY | 898 AGCAGTGAATACGCTCAACCTTTCACATGGAAGGGCTATCTTCACTCTTGAAGCATGTGACA | 957 | |

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| ACCESSION | complete sequence. |
| VERSION | AC006193 |
| KEYWORDS | AC006193.3 GI:4733953 |
| SOURCE | HTG. |
| ORGANISM | Arabidopsis thaliana. |
| | Arabidopsis thaliana |
| | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; |
| | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; |
| | Kosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsida. |
| REFERENCE | 1 (bases 1 to 118335) |
| AUTHORS | Federipiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P., Gonzalez,A., Kremetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S., Luros,S., Schwartz,J., Shinn,P., Toriumi,M., Votskaia,V.S., Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W. |
| JOURNAL | Unpublished |
| REFERENCE | 2 (bases 1 to 118335) |
| AUTHORS | Federipiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P., Gonzalez,A., Kremetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S., Luros,S., Schwartz,J., Shinn,P., Toriumi,M., Votskaia,V., Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W. |
| JOURNAL | Submitted (09-DEC-1998) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA |
| REFERENCE | 3 (bases 1 to 118335) |
| AUTHORS | Federipiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P., Gonzalez,A., Kremetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S., Luros,S., Schwartz,J., Shinn,P., Toriumi,M., Votskaia,V., Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W. |
| JOURNAL | Submitted (04-MAY-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA |
| TITLE | 4 (bases 1 to 118335) |
| JOURNAL | Federipiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P., Gonzalez,A., Kremetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S., Luros,S., Schwartz,J., Shinn,P., Toriumi,M., Votskaia,V., Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W. |
| TITLE | Direct Submission |
| JOURNAL | Submitted (11-JUN-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA |
| REFERENCE | 5 (bases 1 to 118335) |
| AUTHORS | Federipiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Nguyen,M., Lam,B., Southwick,A., Ecker,J., Theologis,A. and Davis,R.W. |
| TITLE | Direct Submission |
| JOURNAL | Submitted (28-MAY-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA |
| COMMENT | On May 4, 1999 this sequence version replaced gi:4678192. |
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TERPPYNNLNRISOTISLSTSSVLRFGCAINVDITTEQVNLVPRPHMLSSYAVI
SSAKYIHQDSVPELTIVSEPSNNMACDPDRHCKYVACCLMTRGDVVPADVNTAVAA

Tel: 81-438-52-3935(ex.2338), Fax: 81-438-52-3934)

FEATURES
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Location/Qualifiers
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[illegible]

| KEYWORDS | HTG: HTGS, PHASE2. |
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| SOURCE | Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA, clone:OJ111_E07. |
| ORGANISM | Oryza sativa (japonica cultivar-group) |
| REFERENCE | Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; Euhartioideae; Oryzaceae; Oryza. |
| REFERENCE | 1 |
| AUTHORS | Sasaki,T., Matsumoto,T. and Yamamoto,K. |
| TITLE | Oryza sativa nipponbare(Ga3) genomic DNA, chromosome 2, BAC clone:OJ111_E07 |
| JOURNAL | Published Only in Database (2001) |
| AUTHORS | 2 (bases 1 to 125422) |
| TITLE | Sasaki,T., Matsumoto,T. and Yamamoto,K. |
| JOURNAL | Direct Submission |
| REFERENCE | Submitted (01-AUG-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannonada 2-1-2, Tsukuba, Ibaraki 305-8602, Japan |
| REFERENCE | (E-mail:tsukubda.ibaraki.affrc.go.jp, URL:http://rgrp.dna.affrc.go.jp/, Tel.:81-298-38-7441, Fax:81-298-38-7468) |
| COMMENT | The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data. |
| FEATURES | NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved. |
| SOURCE | * NOTE: This is a 'working draft' sequence. * This sequence will be replaced * by the finished sequence as soon as it is available and * the accession number will be preserved. |
| BASE COUNT | Location/Qualifiers |
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| | /chromosome="2" |
| | /clone="OJ111_E07" |
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| Db | 15865 AGTTGTGAAGCGAGCTGCGACGCGTGGAGCTCCGGGGCGAGATATCATGTGAGCT 15806 |
| OY | 705 GGTGGCACAGGAGATCTTGGCCCTGACGAACAATCTTTCATCATCATGAGGAGAAATCTCT 764 |
| Db | 15805 GGTGGCATAGGAGACTCGAGCGATCCGAAGAAGATCCCTGAACCTGATGAGCTATCC 15746 |
| OY | 765 TAAAGACATTTGGCATCATATTAACCTCCCTGCTGCTGCTGCTCAACTCTGTATATGTTA 824 |
| Db | 15745 TGAAGAGATATGCGATGCATATTAATCTCCAGACTGGTGTCTTCCTGATTAATGTCA 15686 |
| OY | 825 AGTTGCTCCAAATCCCTGTCACTTCAGACATCA 858 |
| Db | 15685 AAATGGCCGAGTCACTGTCTTTGAGGTAAAAA 15652 |
| RESULT 11 | |
| AF527809/c | 108555 bp DNA linear PLN 12-AUG-2002 |
| LOCUS | Sorghum bicolor clone BAC SB_BB0C234M12 pmp200725 orthologous region. |
| DEFINITION | |
| ACCESSION | AF527809 |
| VERSION | AF527809.1 GI:22208503 |
| KEYWORDS | |
| ORGANISM | Sorghum bicolor |

| | REFERENCE | JOURNAL TITLE | AUTHORS | REFERENCE | | |
|---------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------|----------------------------|
| gene | Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta, Spermatophyta; Magnoliophyta; Liliopsida, Poales; Rosaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum. | 1 (bases 1 to 108553) | Song, R., Liaca, Y. and Messing, J. | Mosaic Organization of Orthologous Sequences In Grass Genomes Unpublished | | |
| CDs | 2 (bases 1 to 108553) | Song, R. and Messing, J. | Direct Submission | Submitted (08-JUL-2002) The Plant Genome Initiative at Rutgers - Mackson Institute, Rutgers University, 190 Frelinghuysen Road, Piscataway, NJ 08873, USA | | |
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| QY 459 CAACCATGTAGGCATCTGAGTCTCTTTCAAGCTCAAGACCAATGCTCTTGGTG 518 | |
| Db 350 TTAACGTACCGGCGCATCACTTACTCCCAACAGTAGTAACGGGCGACGGAATTACTTC 409 | |
| QY 519 CTGCTCAGAGAAATTTGGCTGATAGGTTTCCCTTTCAGTTGCTGACGCTCTACAGCAACCAT 578 | |
| Db 410 CTCCTCGATGTGACGGCCAAAG-----TTTGGCGGTGAGCATGCTTATGCTTGTCTT 460 | |
| QY 579 TCTCTGACGGCCAGTTTATGCTGTGTGCTCCATGAGAGTAGTGAGAGCATATGCTTGACA 638 | |
| Db 461 TTCTCGAGCGTATGTTTCGACATGATTTGGTGGGTGGAAGCAGGGCCCAATGCTTGACA 520 | |
| QY 639 AAGCTAAGTTTGTGGAAGTAGTCTCGGGTAGACAGCACCAGGTGCTATTAATAAATAG 698 | |
| Db 521 AAGCTGTGTTGCCAAGAAATTAATCTGCGGCTGCTGAACACAGGGGCGATTTCTGTGTGG 580 | |
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| DEFINITION | Sequence 3 from Patent WO0104330. | | | | |
| ACCESSION | AX073659 | | | | |
| VERSION | AX073659.1 | GI:12710080 | | | |
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| ORGANISM | Synechocystis sp. PCC 6803 | | | | |
| REFERENCE | Bacteria; Cyanobacteria; Chroococcales; Synechocystis. | | | | |
| AUTHORS | 1 (bases 1 to 974) | | | | |
| TITLE | Hebers,K., Badur,R., Kunze,I. and Geiger,M. | | | | |
| JOURNAL | Identification and overexpression of a dna sequence coding for | | | | |
| | 2-methyl-6-phytylhydroquinone-methyltransferase in plants | | | | |
| | Patent: WO 0104330 A 3 18-JAN-2001; | | | | |
| FEATURES | Sungene GmbH & Co. KGAA (DE) | | | | |
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ORIGIN

Query Match 6.4%; Score 76.6; DB 6; Length 974;
Best Local Similarity 54.7%; Pred. No. 1.5e-08;
Matches 179; Conservative 0; Mismatches 139; Indels 9; Gaps 1;

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Search completed: March 18, 2003, 08:23:32
Job time : 3728 secs

GenCore version 5.1.4-p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 18, 2003, 06:42:05 ; Search time 1529 Seconds
(without alignments)
1751.227 Million cell updates/sec

Title: US-09-857-613A-27

Perfect score: 1189
Sequence: 1 ggcacatggccaccgtgtgtga.....aaaaaaaaaaaaaaaa 1189

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 3 | 459 | 38.6 | 1257 | 21 | AAA29165 |
| 4 | 445.2 | 37.4 | 1293 | 21 | Soybean gamma-toco |
| 5 | 442 | 37.2 | 1071 | 21 | AA298317 |
| 6 | 442 | 37.2 | 1350 | 24 | AA146039 |
| 7 | 442 | 37.2 | 1790 | 20 | AA117789 |
| 8 | 440.4 | 37.0 | 1296 | 21 | AA234022 |
| 9 | 436.2 | 36.7 | 1102 | 21 | AAA29161 |

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| 10 | 353.2 | 29.7 | 1011 | 21 | AAA29155 | Wheat gamma tocoph |
| 11 | 322.2 | 27.1 | 1862 | 22 | AAH44261 | Physcomitrella pat |
| 12 | 310 | 26.1 | 792 | 21 | AAA29151 | Corn gamma tocophe |
| 13 | 147 | 12.4 | 954 | 20 | AA171788 | Synechocystis gamm |
| 14 | 125.8 | 10.6 | 521 | 21 | AAA29152 | Partial gamma toco |
| 15 | 125.8 | 10.6 | 521 | 21 | AAA29162 | Rice gamma-tocophe |
| 16 | 124.8 | 10.5 | 511 | 24 | ABL74098 | Corn tassal-deri |
| 17 | 95.8 | 8.1 | 464 | 21 | AAA29163 | Rice gamma-tocophe |
| 18 | 79.6 | 6.7 | 488 | 22 | AAH44245 | Physcomitrella pat |
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| 20 | 76.6 | 6.4 | 957 | 21 | AA261599 | DNA encoding a met |
| 21 | 76.6 | 6.4 | 957 | 22 | AAH26169 | Synechocystis PCC6 |
| 22 | 76.6 | 6.4 | 957 | 24 | AAH46040 | Synechocystis 2-me |
| 23 | 76.6 | 6.4 | 974 | 22 | AAH26170 | Synechocystis PCC6 |
| 24 | 72.8 | 6.1 | 592 | 21 | AAA29153 | Rice gamma tocophe |
| 25 | 50 | 4.2 | 60 | 21 | AAA29170 | Forward primer to |
| 26 | 47.8 | 4.0 | 1410 | 15 | AAO80524 | Oxidoreducing aver |
| 27 | 47.8 | 4.0 | 7143 | 24 | ABL32983 | Human immune syste |
| 28 | 46.8 | 3.9 | 12381 | 21 | AA238381 | Streptomycetes averm |
| 29 | 45.4 | 3.8 | 752 | 21 | AAH68123 | Human secreted pro |
| 30 | 45.4 | 3.8 | 1923 | 21 | AAA93825 | Modified fibre pro |
| 31 | 45.4 | 3.8 | 6922 | 22 | AAH46533 | Tumour suppressor |
| 32 | 45.4 | 3.8 | 6922 | 24 | AAH61331 | Chemically treated |
| 33 | 45.4 | 3.8 | 6922 | 24 | AAH34510 | Human gene regulat |
| 34 | 45.4 | 3.8 | 6922 | 24 | AAH34510 | Signal transductio |
| 35 | 45.2 | 3.8 | 521 | 22 | AAH34576 | Human colon cancer |
| 36 | 44.2 | 3.7 | 852 | 21 | AAH55802 | S. lavendulae Mtm |
| 37 | 44.2 | 3.7 | 53500 | 21 | AAH55842 | Complete nucleotid |
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| 39 | 43.6 | 3.7 | 2045 | 21 | AAH16314 | Human prostate can |
| 40 | 43.2 | 3.6 | 405 | 22 | AAH18461 | Human polynucleoti |
| 41 | 43.2 | 3.6 | 466 | 23 | ABV05510 | Human prostate exp |
| 42 | 43.2 | 3.6 | 475 | 23 | ABV48025 | Human prostate exp |
| 43 | 43.2 | 3.6 | 556 | 23 | ABV40063 | Human prostate exp |
| 44 | 43.2 | 3.6 | 556 | 23 | ABV40163 | Human prostate exp |
| 45 | 43.2 | 3.6 | 556 | 23 | ABV42105 | Human prostate exp |

ALIGNMENTS

| | | |
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| XX | | |
| DE | Soybean gamma-tocopherol methyltransferase cDNA (clone sahlc.pk004.92). | |
| XX | | |
| KW | Vitamin E: alpha-tocopherol: biosynthesis; enzyme; inhibitor; herbicide; | |
| KW | gamma-tocopherol methyltransferase; ss. | |
| XX | | |
| OS | Glycine max. | |
| XX | | |
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| PD | 08-JUN-2000. | |
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| PF | 02-DEC-1999; | 99WO-US28588. |
| XX | | |
| PR | 03-DEC-1998; | 98US-0110781. |
| XX | | |
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| XX | | |
| XX | Arabidopsis gamma-t | |
| XX | Arabidopsis gamma-t | |
| XX | Arabidopsis thaila | |
| XX | Cahoon RE, Coughlan SJ, Miao G, Rafalski JA; | |
| XX | | |

xx Claim 3; Page 52; 82pp; English.

cc AAA29151-69 encode vitamin E (alpha-tocopherol) biosynthetic enzymes or
cc their fragments. The cDNA clones were identified by BLAST searches based
cc on similarity to *Synechocystis* sp. and *Arabidopsis thaliana* vitamin E
cc biosynthetic enzymes. The enzymes are useful for synthesizing
cc plastoquinones or tocopherols (especially vitamin E). Vitamin E is
cc required for plant growth, therefore the enzymes may be used for the
cc discovery of new herbicides. The enzymes can be used in methods to
cc evaluate potential inhibitors, which may have use as herbicides.
cc Additionally, transgenic expression of, e.g., gamma-tocopherol
cc methyltransferase affords the ability to manipulate tocopherol levels as
cc desired for a particular application.

xx Sequence 1331 BP; 373 A; 293 C; 301 G; 364 T; 0 other;

Query Match 80.2%; Score 953; DB 21; Length 1331;

Best Local Similarity 100.0%; Pred. No. 1.5e-250;

Matches 953; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 2 GACATGGCCACCGTGTGATGATCCCAATCTCATGATCCACATCCACAGTTCCT 61
DB 3 GACATGGCCACCGTGTGATGATCCCAATCTCATGATCCACATCCACAGTTCCT 62
QY 62 TCCCAATCCCTCCGACATTTTGGCCAGAAATCCGGTCCGACAGGCTGGGCTCTATT 121
DB 63 TCCCAATCCCTCCGACATTTTGGCCAGAAATCCGGTCCGACAGGCTGGGCTCTATT 122
QY 122 CGGCGATCGGACGACGATCGAGAGAGGAGATAGTATTTGAGAGCAGAACCGAAGAAG 181
DB 123 CGGCGATCGGACGACGATCGAGAGAGGAGATAGTATTTGAGAGCAGAACCGAAGAAG 182
QY 182 GATGCAAGAAAGACCTGACAGAGGAATCGCAGAGTTTACGACAGTCTGTGGCTTA 241
DB 183 GATGCAAGAAAGACCTGACAGAGGAATCGCAGAGTTTACGACAGTCTGTGGCTTA 242
QY 242 TGGGAGAAATTTGGGGGACACACATGACCATGCTTTATGACTCGGATTCACATGTT 301
DB 243 TGGGAGAAATTTGGGGGACACACATGACCATGCTTTATGACTCGGATTCACATGTT 302
QY 302 TCGCTTTGGATCATGCTGCTCTCAGATCCGAATGATCCAGAGTCTCTCGCTTGGCC 361
DB 303 TCGCTTTGGATCATGCTGCTCTCAGATCCGAATGATCCAGAGTCTCTCGCTTGGCC 362
QY 362 TCTGTTTCTGAGAGAGCTGTAATATGCCCCAAGAGTATAGTTGTTGGTGTGCATA 421
DB 363 TCTGTTTCTGAGAGAGCTGTAATATGCCCCAAGAGTATAGTTGTTGGTGTGCATA 422
QY 422 GGTGGAGAGCTAGATACCTGGCCAAAGAAATTTGAGCAACAGTGTAGGATCAGCTG 481
DB 423 GGTGGAGAGCTAGATACCTGGCCAAAGAAATTTGAGCAACAGTGTAGGATCAGCTG 482
QY 482 AGTCTGTTCAAGCTCAAGAGCAAAATGCTTGTCTGCTCAGCTCAAGATTTGGATTAAG 541
DB 483 AGTCTGTTCAAGCTCAAGAGCAAAATGCTTGTCTGCTCAGCTCAAGATTTGGATTAAG 542
QY 542 GTTTCCTTTACAGTCTCTCAAGCTCTACAGCAACATTTCTCTACGCGCCAGTTTGATCTG 601
DB 543 GTTTCCTTTACAGTCTCTCAAGCTCTACAGCAACATTTCTCTACGCGCCAGTTTGATCTG 602
QY 602 GTTGGTCCATGAGAGAGTGGAGAGCATATGCCGACAAAGCTTAAGTTTGTGGAGGTTA 661
DB 603 GTTGGTCCATGAGAGAGTGGAGAGCATATGCCGACAAAGCTTAAGTTTGTGGAGGTTA 662
QY 662 GCTCGGTAGACAGACAGAGTGGCATTAATATAGTAACATGTTGCCACAGAGATCTT 721
DB 663 GCTCGGTAGACAGACAGAGTGGCATTAATATAGTAACATGTTGCCACAGAGATCTT 722
QY 722 GGCCTGACGAACATCTTACATCCATGGGAGCAAGATCTTTAAAGAAGATTTGGCAT 781
DB 723 GGCCTGACGAACATCTTACATCCATGGGAGCAAGATCTTTAAAGAAGATTTGGCAT 782

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QY 782 GCATATTACCTCCCTGCTGCTGCTCAACTCTGATATGATTAAGTGTCTCCATCCCTG 841
DB 783 GCATATTACCTCCCTGCTGCTGCTCAACTCTGATATGATTAAGTGTCTCCATCCCTG 842
QY 842 TCACTTACAGACATCAAGTCACAGAAATTTGCTGCTTGTGCTCCATTGGCCAGCA 901
DB 843 TCACTTACAGACATCAAGTCACAGAAATTTGCTGCTGCTGCTGCTCCATTGGCCAGCA 902
QY 902 GTGATACGCTCAAGCTTTCACATGAGAAAGGCTATCTTACCTGAGCAGTGG 954
DB 903 GTGATACGCTCAAGCTTTCACATGAGAAAGGCTATCTTACCTGAGCAGTGG 955

```

RESULT 3

AAA29165

ID AAA29165 standard; cDNA; 1257 BP.

XX AAA29165;

XX 12-SEP-2000 (first entry)

XX Soybean gamma-tocopherol methyltransferase cDNA.

XX Vitamin E: alpha-tocopherol; biosynthesis; enzyme; inhibitor; herbicide;

XX gamma-tocopherol methyltransferase; ss.

XX Triticum aestivum.

XX Key Location/Qualifiers

XX CDS 18..1118

XX /tag= a

XX /transl_except= (pos:30..32, aa:Xaa)

XX /transl_except= (pos:150..152, aa:Xaa)

XX /product= gamma-tocopherol methyltransferase

XX /note= "Xaa is not defined"

XX W0200032757-A2.

XX 08-JUN-2000.

XX 02-DEC-1999: 99WO-US26588.

XX 03-DEC-1998: 98US-0110781.

XX (DUPO) DU PONT DE NEMOURS & CO E. I.

XX Cahoon RE, Coughlan SJ, Miao G, Rafalski JA;

XX MPI: 2000-412309/35.

XX P-PSDB: AAY96473.

XX polynucleotide encoding a vitamin E biosynthetic enzyme polypeptide

XX such as gamma tocopherol methyltransferase, useful for synthesizing

XX vitamin E or as a target for design and discovery of herbicides

XX Claim 3; Page 66; 82pp; English.

cc AAA29151-69 encode vitamin E (alpha-tocopherol) biosynthetic enzymes or
cc their fragments. The cDNA clones were identified by BLAST searches based
cc on similarity to *Synechocystis* sp. and *Arabidopsis thaliana* vitamin E
cc biosynthetic enzymes. The enzymes are useful for synthesizing
cc plastoquinones or tocopherols (especially vitamin E). Vitamin E is
cc required for plant growth, therefore the enzymes may be used for the
cc discovery of new herbicides. The enzymes can be used in methods to
cc evaluate potential inhibitors, which may have use as herbicides.
cc Additionally, transgenic expression of, e.g., gamma-tocopherol
cc methyltransferase affords the ability to manipulate tocopherol levels as
cc desired for a particular application.

xx Sequence 1257 BP; 299 A; 370 C; 343 G; 243 T; 2 other;

Query Match 38.6%; Score 459; DB 21; Length 1257;

Best Local Similarity 70.9%; Pred. No. 2.6e-115;

| Query | Best Local Similarity | Score | DB | Length |
|--------------|-----------------------|--------|------|--------|
| 01-SEP-1999; | 9905-0151930. | 37.4%; | 21; | 1293; |
| 07-SEP-1999; | 9905-0152363. | 70.5%; | 11; | |
| 10-SEP-1999; | 9905-0153070. | 0; | 253; | 9; |
| 13-SEP-1999; | 9905-0153758. | | | Gaps |
| 15-SEP-1999; | 9905-0154018. | | | |
| 16-SEP-1999; | 9905-0154039. | | | |
| 20-SEP-1999; | 9905-0154779. | | | |
| 22-SEP-1999; | 9905-0155139. | | | |
| 23-SEP-1999; | 9905-0155486. | | | |
| 24-SEP-1999; | 9905-0155659. | | | |
| 28-SEP-1999; | 9905-0156458. | | | |
| 29-SEP-1999; | 9905-0156596. | | | |
| 04-OCT-1999; | 9905-0157117. | | | |
| 05-OCT-1999; | 9905-0157753. | | | |
| 06-OCT-1999; | 9905-0157865. | | | |
| 07-OCT-1999; | 9905-0158028. | | | |
| 08-OCT-1999; | 9905-0158232. | | | |
| 12-OCT-1999; | 9905-0158369. | | | |
| 13-OCT-1999; | 9905-0159293. | | | |
| 13-OCT-1999; | 9905-0159294. | | | |
| 13-OCT-1999; | 9905-0159295. | | | |
| 14-OCT-1999; | 9905-0159329. | | | |
| 14-OCT-1999; | 9905-0159330. | | | |
| 14-OCT-1999; | 9905-0159331. | | | |
| 14-OCT-1999; | 9905-0159637. | | | |
| 14-OCT-1999; | 9905-0159638. | | | |
| 18-OCT-1999; | 9905-0159584. | | | |
| 21-OCT-1999; | 9905-0160741. | | | |
| 21-OCT-1999; | 9905-0160767. | | | |
| 21-OCT-1999; | 9905-0160768. | | | |
| 21-OCT-1999; | 9905-0160770. | | | |
| 21-OCT-1999; | 9905-0160814. | | | |
| 21-OCT-1999; | 9905-0160815. | | | |
| 22-OCT-1999; | 9905-0160980. | | | |
| 22-OCT-1999; | 9905-0160981. | | | |
| 22-OCT-1999; | 9905-0160989. | | | |
| 25-OCT-1999; | 9905-0161404. | | | |
| 25-OCT-1999; | 9905-0161405. | | | |
| 25-OCT-1999; | 9905-0161406. | | | |
| 25-OCT-1999; | 9905-0161359. | | | |
| 26-OCT-1999; | 9905-0161360. | | | |
| 26-OCT-1999; | 9905-0161361. | | | |
| 28-OCT-1999; | 9905-0161920. | | | |
| 28-OCT-1999; | 9905-0161992. | | | |
| 28-OCT-1999; | 9905-0161993. | | | |
| 29-OCT-1999; | 9905-0162142. | | | |

| Query Match | 37.4%; | Score 445.2; | DB 21; | Length 1293; |
|-----------------------|--------------|---------------------|-----------------|--------------|
| Best Local Similarity | 70.5%; | Pred. No. 1.6e-111; | | |
| Matches 626; | Conservative | 0; | Mismatches 253; | Indels 9; |
| | | | | Gaps 2 |

| Query | 187 | CAGAAGAAAGCTGCAGAGGAATGCCAGAGTTTACGACGAGCTCTGGCTTANGGA | 246 |
|-------|-----|---------------------------------------------------------------|-----|
| Db | 233 | CACGTAGGGCGCTAAGAAAGAAATAGCGGCTTCTACAAATGAAACTTCGGGTTGTGGGA | 292 |
| Qy | 247 | GAAACATTTGGGGCGACCATATGCACATGGCTTTATNGATCGGATTTCCACTGTTCCGT | 306 |
| Qy | 293 | AGAGATTTGGGGGATCATATGTCATATGGCTTTATNGACCCGTGATCTTCTGTTCACT | 352 |
| Db | 307 | TTGGAGTACATCGT-----GCTGCTAGATCCGAATGCAGAGTATAGTTGATGTTGGGTGCG | 360 |
| Qy | 353 | TTTGTGATTTGTCACAGAGAGCTAGATCCGTATGATTAAGAGAGTCTCTCGTTTGGC | 412 |
| Db | 361 | CTCTGTTTTC---TGAGAGCGGTAGTAAATGCGCCCAAGAGTATAGTTGATGTTGGGTGCG | 417 |
| Qy | 413 | CGGTGTACTGATGAGAGAGAGAGAAAGATAAAGAGTATGATGATGTTGGGTGCG | 472 |
| Db | 418 | CATAGTGCAGCTCTAGATACCTGGCCCAAGAAATTTGGAGCAACAGTGTAGGCATCAC | 477 |
| Qy | 473 | GATTTGAGGAGAGCTCAAGATATCTTGCTCTAAATTTGGAGCTGAATGCAATGGCATTAC | 532 |
| Db | 478 | TTGTGAGTCCCTGTCAGAGCTCAAGAGCAATGCTTGTGCTGCTCAGAGATTTGGCTGA | 537 |

Db 533 TCTGACCCCTGTCAGCCCAAGAGACCAGCATGATCTCGCGCTGCTCAATCACTGCTCA
 Oy 538 TAAGTTTCTTTGAGTTGTCAGCGCTCTACAGCAACATTTCTGTGACGGCACTTTGA 597
 Db 593 TAAGCTTCTTCCAAAGTTGGAGATCGTTGATGACCATTTGCAAGATGAAAAATTCGA 652
 Oy 598 TCTGCTGTGTCATGAGAGTGAAGACATATGCTGACAAAGCTAGATTGTTGGAGA 657
 Db 653 TCTAGTGTGTCATGAGAGATGTTGATGCTGACAAAGCAAGTTGTTAAAGA 712
 Oy 658 GTTAGCTGGGTAGACAGACAGTGCATTAATAATAATAGTACATGTGTCACAGGGA 717
 Db 713 GTTGATGCTGTGCGCTCCAGAGGTAGATATAATAGACATGTGTCATAGAAA 772
 Oy 718 TCTTGCCCTTGACAGCAATCTTACATCATGAGAGCAAGTCTCTTAAGAAATTTG 777
 Db 773 TCTATCTGCGGGGAGAGAGCTTTGACCGCTGGAGCAAAACATCTTGACAAATCTG 832
 Oy 778 CGATGATATTAATCTCCCTGCTGCTGCTCACTTGTATGTTAGTTGCTCCAATC 837
 Db 833 TAAGACGTTCTATCTCCCGGCTTGCTGCTCCAGCATGATATGTTCAACTTCTCAATC 892
 Oy 838 CTTGCTACTTACAGACATCAAGTCAAGAAATGTTGCTGCTTGTGCTCAATTTTGGCC 897
 Db 893 CCATTCTCTCCAGATATTAAGTGTGCGGATGTGTCAGAGAACGTAGCTTCTTGCGCC 952
 Oy 898 AGCATGTATGCTGACGCTTACATGAGAGGCTATCTTACCTTACCTTGAGAGTGACA 957
 Db 953 TCGGATTAATGAGACTGATTAACATGAGAGGCTTGTGCTGCTTCTGATGAGAT 1012
 Oy 958 AAAACGATTAAGAGAGCTTTGCTATGCTCAATGATAGAGGATCAAGAAAGATCT 1017
 Db 1013 GAAAGATTAAGAGAGATTTGACATGCTCAATGATGATGATGAGTTGACAAAGAGTGT 1072
 Oy 1018 AATTAAGTTTCCATCATATCATGCTGAAACCTGAAATTAATGAGAG 1065
 Db 1073 CATTAAGTTTGTATCATCTGCTCCAGAGACCTCACTAAGTCTTAAG 1120

RESULT 5

AA298317
 ID AA298317 standard; DNA; 1071 BP.

AA298317;

14-JUN-2000 (first entry)

A. thaliana gene involved in environmental stress tolerance.

Environmental stress; plant; transgenic plant; anaerobic; flooding; cold;
 dehydration; drought; heat stress; salinity; osmotolerance; ds.

Arabidopsis thaliana.

W0200008187-A2.

17-FEB-2000.

04-AUG-1999; 99WO-EP05652.

04-AUG-1998; 98EP-0202634.

(VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.

Lee JH, Verbruggen N;

WPI; 2000-205726/18.

P-PSDB; AAY77937.

Isolation of polynucleic acids useful for producing transgenic plant by
 isolating genes involved in tolerance to environmental stress

Claim 4; Page 130-132; 312pp; English.

The invention relates to isolation of coding sequences and/or genes
 involved in tolerance to environmental stress in plants. The sequences
 (AA298305-298365) are useful for producing a transgenic plant having
 enhanced tolerance or resistance to environmental stress conditions such
 as anaerobic, flooding, cold, dehydration, drought, heat stress or
 salinity. This is useful for producing improved yield, growth,
 development and productivity under environmental stress conditions, and
 also provides growth of crops in areas where they cannot grow without
 the induced osmotolerance. Sequences AA298305-365 represent
 polynucleotide sequences from A. thaliana that are involved in
 environmental stress tolerance.

Sequence 1071 BP; 277 A; 229 C; 270 G; 295 T; 0 other:

Query Match 37.2%; Score 442; DB 21; Length 1071;

Best Local Similarity 70.3%; Pred. No. 1.1e-110;

Matches 624; Conservative 0; Mismatches 255; Indels 9; Gaps 2;

Oy 187 CAAGAAAGAGCTGCAGAAAGGAAATGCGAGATTTACGACGAGTGTGCTTATGGA 246
 Db 176 CACTAGGCGCTTAAGAAAAAGAAATAGCGGATTCACATGAACCTTGGGTTTGGA 235
 Oy 247 GAACATTTGGGGGAGACACATGACCATGAGCTTTATGATGCTGATTCACATGTTGCT 306
 Db 236 AGAGATTTGGGAGATCATATGCTATGCTTTTATGACCTGATTTCTTCTTCAACT 295
 Oy 307 TTGAGATCATCTGCT-----GCTGCTCAGATCCGAATGATCCAGAGTCTTCTGCTTGC 360
 Db 296 TTTGATTTGCTGTCACAAAGAGCTCAGATCCGATGATGAAGATGCTCTCGTTTGGC 355
 Oy 361 CTCTCTTTC---TGAGAGAGCTAGTAAATGAGCCCAAGAGTATAGTATGTTGGGTGAG 417
 Db 356 CGGTCTTACTGATGAGAGAGAGAGAGAAAAAGTAAAGATGAGATGGGTGGTGG 415
 Oy 418 CATAGTGGACGCTTAGATACCTGAGCAAGAAATTTGGAGCAACAGTGAAGATCAGC 477
 Db 416 GATTGGAGAGAGCTCAAGATATCTTGGCTCTTAATTTGGAGCTGAATGATGCTTTCAC 475
 Oy 478 TCTGAGCTCTGTCAGCTCAAGAGCAAAAGCTCTTGTGCTGCTCAAGATTTGCTGCA 537
 Db 476 TCTCAGCCCTGTCAGGCCCAAGAGACCAATGATCTCGGGCTGCTCAATCACTCTGCA 535
 Oy 538 TAAGTTTCTTTGAGTTGCTGAGGCTCTACAGACCATTTCTGACGGCACTTTGA 597
 Db 536 TAAGCTTCTTCCAAAGTTGCGGATCGTTGATAGCGATTGCAAGATGGAATTTGA 595
 Oy 598 TCTGCTGTGTCATGAGAGAGTGAAGAGCATATGCTGACAAAGCTAAGTTTGGAGA 657
 Db 596 TCTAGTGTGTCATGAGAGAGTGTGAGCATATGCTTGAAGGCAAGTTTGTAAAGA 655
 Oy 658 GTTAGCTGGGTAGAGACACAGTGCATTAATAATAATAGTACATGTGTCACAGGGA 717
 Db 656 GTTGATGAGTGTGCGGCTCCAGGAGTGAATATAATAGATGATGCTGCAATAGAA 715
 Oy 718 TCTTGCCCTTGACAGCAATCTTACATCATGAGAGCAAGTCTCTTAAGAAATTTG 777
 Db 716 TCTATCTGCGGGGAGAGAGCTTTGACCGCTGGAGCAAAACATCTTGAGCAAAATCTG 775
 Oy 778 CGATGATATTAATCTCCCTGCTGCTGCTCACTTGTATGTTAGTTGCTCCAATC 837
 Db 776 TAAGACGTTCTATCTCCCGGCTTGCTGCTCCAGCATGATATGTTCAACTTCTCAATC 835
 Oy 838 CTTGCTACTTACAGACATCAAGTCAAGAAATGCTGCTGCTTGTGCTCAATTTTGGCC 897
 Db 836 CCATTCTCTCCAGATATTAAGTGTGCGGATGTGCAAGAAAGTCTCTTCTTGCGCC 895
 Oy 898 AGCATGTATGCTGACGCTTACATGAGAGGCTATCTTACCTTGAAGAGTGACA 957
 Db 896 TCGGATTAATGAGACTTATTAACATGGAAGGCTTGTGCTGCTTCTGATGAGAT 955
 Oy 958 AAAACGATTAAGAGAGCTTTGGCTATGCTCAATGATAGAGGATCAAGAAAGATCT 1017

Db 956 GAAAGATTAAGAGCATGACAAATCCATGATGATTGAAGTTACAGAAAGGTGT 1015
 QY 1018 AATTAGTTGGCATTCATTACATGTCGAAACCGATTAATGAGAG 1065
 Db 1016 CATTAGTTGGTATCATCTGCGCAAGCCACTTAAGTCTAAAG 1063

RESULT 6
 AAL46039
 ID AAL46039 standard; cDNA: 1350 BP.
 AC AAL46039;
 XX 11-JUL-2002 (first entry)
 DE A thaliana gamma-tocopherol methyltransferase cDNA.
 XX Vitamin E; homogenisate; HG; homogenisate-1,2-dioxygenase; HGD;
 KW maleylacetoacetate-isomerase; MAAI; fumarylacetoacetate-hydrolase; FAAH;
 KW transgenic; nutrition; antioxidant; cardiovascular disease; cancer;
 KW immune system; generalised age-related degeneration; animal feed;
 KW meat quality; cosmetics; growth regulator; herbicide; cardiant;
 KW cytosolic; immunostimulant; enzyme; gene; ss.
 XX Arabidopsis thaliana.
 OS
 FH Key Location/Qualifiers
 FT 63..1109
 FT CDS /tag="a
 FT /product="gamma-tocopherol methyltransferase"
 XX MO200231173-A2.
 XX 18-APR-2002.
 PD 18-SEP-2001; 2001MO-EPI0779.
 PE 18-SEP-2001; 2000DE-1046462.
 XX 19-SEP-2000; 2000DE-1046462.
 PR (SUNG-) SUNGENE GMBH & CO KGAA.
 PA
 PI Gelger M, Ebneth M, Kunze I:
 XX WPI: 2002-362682/39.
 DR P-PSDB: AAO17426.
 XX
 PT Increasing Vitamin E production, useful in human or animal nutrition,
 PT comprises reducing activity of enzymes that metabolize homogenisate,
 XX
 PS Disclosure: Page 83-85; 98pp; German.
 XX
 CC The present invention relates to a method of producing Vitamin E
 CC involving modulating the synthesis of vitamin E by reducing decomposition
 CC of homogenisate (HG) by reducing the activity of
 CC homogenisate-1,2-dioxygenase (HGD), maleylacetoacetate-isomerase (MAAI)
 CC and/or fumarylacetoacetate-hydrolase (FAAH). The method is used to
 CC produce transgenic organisms that are useful in animal and human
 CC nutrition and for the isolation of vitamin E. Vitamin E is a fat-soluble
 CC antioxidant with a protective effect against cardiovascular disease and
 CC cancer. It also stimulates the immune system and may prevent generalised
 CC age-related degeneration. When used in animal feeds, it improves quality
 CC and storability of meat and can also be used in cosmetics. Also
 CC antibodies raised against the 3 specified enzymes are useful in screening
 CC for specific inhibitors, potentially useful as growth regulators, e.g.
 CC herbicides. The present sequence is the A thaliana gamma-tocopherol
 CC methyltransferase cDNA.
 XX
 SQ Sequence 1350 BP; 374 A; 278 C; 314 G; 384 T; 0 other;

Query Match 37.2%; Score 442; DB 24; Length 1350;
 Best Local Similarity 70.3%; Pred. No. 1..2e-110;
 Matches 624; Conservative 0; Mismatches 255; Indels 9; Gaps 2;

QY 187 CAGAGAGCTGACAGAGGAATCGCAGAGTTTACAGAGCTGCTGGCTTATGGA 246
 Db 230 CACTAGAGCGCTTAAGAAAGGAATAGCGAGTTCTACAAATGAACCTCGGGTTGTGGA 289
 QY 247 GACATTTGGGGCGACACATGACACATGCTTTTATGACTCGGATTCACATGTTTGGT 306
 Db 290 AGAGATTTGGGAGATCATATGATTCATTTGGTTTATGACCCCTGATCTTCTGTTCACT 349
 QY 307 TTTGAGTCATGCT-----GCTGCTCAGATCCGATGATCCAGAGTCTCTGCTTTGC 360
 Db 350 TTTGATTTCTGCTGTCACAAAGAGCTCAGATCCGATGATGATGAAAGTCTCTCCCTTTCGC 409
 QY 361 CTCTGTTTCT---TGAGAGCGCTAGTAAATGCCCCCAAGATATAGTATGTTGGGTGG 417
 Db 410 CGGTGTACTGATGATGAAGGAGGAGGAGAAATAAGTAAGTAAGTATGATGGATGGGTGG 469
 QY 418 CATAGGTGCGACGCTCTATACCTGCGCCAGAAATTTGAGCAACAGTATGAGCATAC 477
 Db 470 GATTGAGAGAGCTCAAGATATCTTGGCTTAATTTGAGCTGAATGCAATGGCATTTAC 529
 QY 478 TCTGAGTCTCTTCAAGCTCAAGAGCAAAATGCTCTGCTGCTCAAGATTTGGCTGA 537
 Db 530 TCTGAGCCCTGTTCAAGGCCAAGAGCAATGATCTCGCGCTGCAATGACTCTCA 589
 QY 538 TAAGGTTCTTTTCAAGTTGCTGACGCTCTACAGCAACCATTTCTGACGGCCAGTTGA 597
 Db 590 TAAGGTTCTTTTCAAGTTGCTGACGCTCTACAGCAACCATTTCTGACGGCCAGTTGA 649
 QY 598 TCTGCTGCTGCTGCTGAGAGTGGAGCATATGCTGCTCAAGAGTATGTTTGGAGA 657
 Db 650 TCTAGTGTGCTGATGAGAGTGGAGCATATGCTGCTCAAGAGTATGTTTGGAGA 709
 QY 658 GTTAGCTGCTGAGAGCAGCAGTGCATTTAAATAGTATGATGATGCTGCTGAGAGGA 717
 Db 710 GTTGTGACTGTGCGGGCTCCAGAGATGATTAATATGATGATGCTGCTGAGAGGA 769
 QY 718 TCTTGCCCTGAGCAATCTTATCATCAGAGAGCAAGATCTTAAATGAATTTG 777
 Db 770 TCTATCTGCGGGGAGAGAGTTCAGCCGCTGCGGAGCAAAATCTTGGAGCAAAATCTG 829
 QY 778 CGATGATATATACCTCCCTGCTGCTGCTCACTTGTATGTTAAGTCTGCTCAATC 837
 Db 830 TAAGAGCTTCTATCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 889
 QY 838 CCGTCACTTCAAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 897
 Db 890 CCAATTTCTCAAGATATTAAGTGGATGATGATGATGATGATGATGATGATGATGATG 949
 QY 898 AGCAGTATACGCTCAGCTTCAATGATGATGATGATGATGATGATGATGATGATGATG 957
 Db 950 TCGGTTTATACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1009
 QY 958 AAAACGATTAAGAGAGCTTGGCTATGCTGATGATGATGATGATGATGATGATGATGAT 1017
 Db 1010 GAAAGATTAATTAAGAGAGCTTGGCTATGCTGATGATGATGATGATGATGATGATGATG 1069
 QY 1018 AATTAGTTGGCATTCATTACATGTCGAAACCGATTAATGAGAG 1065
 Db 1070 CATTAGTTGGTATCATCTGCGCAAGCCACTTAAGTCTAAAG 1117

RESULT 7
 AAX17789
 ID AAX17789 standard; DNA: 1790 BP.
 AC AAX17789;
 XX 21-MAY-1999 (first entry)
 DE Arabidopsis gamma-tocopherol methyltransferase encoding gene.
 XX
 XX Gamma-tocopherol methyltransferase; gamma-TMT; SDR0089; 165H577; meat;
 KW transgenic plant; alpha-tocopherol; gamma-tocopherol; forage plant; ds.

```

XX OS Arabidopsis sp.
XX FH Key Location/Qualifiers
XX CDS 207..1253
XX FT /tag= "165H577"
XX FT /gene= "165H577"
XX FT /product= "gamma-TMT"
XX PN W09904622-A1.
XX PD 04-FEB-1999.
XX PF 22-JUL-1998; 98WO-0515137.
XX PR 17-JUL-1998; 98US-0053819.
XX PR 25-JUL-1997; 97US-0053819.
XX PR 26-JAN-1998; 98US-0072497.
XX PA (UTRE-) UNIV NEVADA.
XX PI Dellapenna D, Shintani DK;
XX DR MPI: 1999-142458/12.
XX DR P-PSDB; AAM95017.
XX PT Newly isolated DNA fragment comprising a 14C-tocopherol (vitamin E)
XX PT methyltransferase coding sequence - useful for producing
XX PT  $\alpha$ -tocopherol, and transgenic plants, seeds and oils with an altered
XX PT tocopherol profile
XX PS Claim 2; Page 36-38; 46pp; English.
XX XS
XX CC The invention provides DNA sequences encoding gamma-tocopherol
XX CC methyltransferases (gamma-TMT). The gamma-TMT encoding genes SLR0089
XX CC and 165H577 are isolated from Synchocystis and Arabidopsis species
XX CC respectively. The DNA fragments are useful for producing transgenic
XX CC plants containing a higher alpha-tocopherol:gamma-tocopherol ratio. They
XX CC are also useful for producing alpha-tocopherol and plants with increased
XX CC gamma-tocopherol, which may be useful in certain industries such as the
XX CC meat industry e.g. for developing forage plants to feed animals. The
XX CC production of transgenic plants (and seeds) with a higher alpha-
XX CC tocopherol:gamma-tocopherol ratio, using the gamma TMTs, will increase
XX CC the level of alpha-tocopherol in the human diet, in addition to enhancing
XX CC the stability and shelf life of plants and plant products. Increased
XX CC levels of alpha-tocopherol will also increase meat quality and extend
XX CC shelf life of post-processed meat products. Plants with a higher alpha-
XX CC tocopherol:gamma-tocopherol ratio may also produce advantageous
XX CC phenotypes. The present sequence represents the 165H577 gene encoding the
XX CC Arabidopsis gamma-TMT.
XX SQ Sequence 1790 BP; 474 A; 404 C; 436 G; 476 T; 0 other;
XX
XX Query Match 37.28; Score 442; DB 20; Length 1790;
XX Best Local Similarity 70.38; Pred. No. 1.4e-110;
XX Matches 624; Conservative 0; Mismatches 255; Indels 9; Gaps 2;
XX
OY 187 CAAGAGAGAGCTCAGAGAGGATCCAGAGTTTACGACGAGTCTGCGCTTATGGA 246
DB 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 374 CACTGAGGGCGCTAAGAAAAGGATACGGAGTTCTACATGAAGAACTCGGGTTGTGGGA 433
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OY 538 TAAAGTTTCCCTTTCAGGTTGCTGACGCTCTACACCAACCATCTCTCAAGCCGCAATTGA 597
DB 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
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OY 598 TCTGCTGTGTGTTCATGAGAGATGAGAGCATATGCTCTGACAAAGCTTAAGTTTGTGAGA 657
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DB 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
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XX
XX RESULT 8
XX AAC34022
XX ID AAC34022 standard; DNA; 1296 BP.
XX AC AAC34022;
XX AC
XX DT 17-OCT-2000 (first entry)
XX XX
XX DB Arabidopsis thaliana DNA fragment SEQ ID NO: 5167.
XX KM Hybridisation assay; genetic mapping; gene expression control;
XX KM protein identification; signal transduction pathway;
XX KM metabolic pathway; promoter; termination sequence; ss.
XX OS Arabidopsis thaliana.
XX PN EP1033405-AZ.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-0301439.
XX PR 25-FEB-1999; 99US-0121825.
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PR 29-OCT-1999; 99US-0162142.

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Query Match 37.0%; Score 440.4; DB 21; Length 1296;
Best Local Similarity 70.2%; Pred. No. 3.2e-110;

Matches 623; Conservative 0; Mismatches 256; Indels 9; Gaps 2;

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OY 187 CAGAGAGAGCTGCAGAGGAAATGCGAGAGTTTACGACGCTGCTGCTTATGCGA 246
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OY 247 GAACCTTTGGGGCCACCATGACATGCGCTTTATGCTGCGATTCACCTGTTCCGT 306
DB 295 AGAGATTTGGGAGATCATGATGATGATGATGATGATGATGATGATGATGATGATG 354
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DB 775 TCTATCTGCGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 834

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RESULT 9
AAA29161
ID AAA29161 standard; cDNA; 1102 BP.
XX
AC AAA29161;
XX
DT 12-SEP-2000 (first entry)
XX
DE Corn gamma-tocopherol methyltransferase cDNA.
XX
KW Vitamin E; alpha-tocopherol; biosynthesis; enzyme; inhibitor; herbicide;
XX gamma-tocopherol methyltransferase; ss.
XX
Zea mays.
XX
FH Key Location/Qualifiers
FT CDS 1..1059
FT FT /*tag= a
FT FT /product= gamma_tocopherol_methyltransferase
FT FT /transl_except= (pos:454..456, aa:xa)
FT FT /note= "Xaa not defined."
PN WO200032757-A2.
PD 08-JUN-2000.
XX
PF 02-DEC-1999; 99WO-US28588.
XX
PR 03-DEC-1998; 98US-0110781.
XX
PA (DUPO ) DU PONT DE NEMOURS & CO E. I.
XX
PI Cahoon RE, Coughlan SJ, Miao G, Rafalski JA;
XX WPI: 2000-412309/35.
XX DR P-PSDB; AAY96469.
XX
PT Polynucleotide encoding a vitamin E biosynthetic enzyme polypeptide
PT such as gamma tocopherol methyltransferase, useful for synthesizing
PT vitamin E or as a target for design and discovery of herbicides
XX
PS Claim 3; Page 60; 82pp; English.
XX
CC AA29151-69 encode vitamin E (alpha-tocopherol) biosynthetic enzymes or
CC their fragments. The cDNA clones were identified by BLAST searches based
CC on similarity to Synecchocystis sp. and Arabidopsis thaliana vitamin E
CC biosynthetic enzymes. The enzymes are useful for synthesizing
CC plastoquinones or tocopherols (especially vitamin E). Vitamin E is
CC required for plant growth, therefore the enzymes may be used for the
CC discovery of new herbicides. The enzymes can be used in methods to
CC evaluate potential inhibitors, which may have use in herbicides.
CC Additionally, transgenic expression of, e.g. gamma-tocopherol

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Db 121 AGGCGCTCGCCTTCGCCGCGGCCGAGATCCGACAAACCAACCAACGATTTGTT 180
Oy 405 ATTTGGGTGTGGCATAAGTGGCAGCTCTAGATACCTGGCCAAAGAAATTTGGACACCA 464
Db 181 ATGTTGATGCGGATCGGTGTAGCTCAAGATCTGGGCGCAAAATATGAGACAA 240
Oy 465 GTGTAGGCACTGACTGCTGCTGCTCAAGACCAATGCTTGTGCTGCTC 524
Db 241 TGTCTGGAGTACATGACCCAGTGCAGAGAGAGAGAAATGCTCGGCGAGCG 300
Oy 525 AAGATTTGGCTGATAGTTCTTTTCTGAGTTGCTGAGCTGCTGACCAACCTTCTG 584
Db 301 AAGGGGTGTCCGACAAAGTTCTTTTCTGATTTCTGCTGAGGACCACTTTCTG 360
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Oy 704 TGTGTCACAGGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 763
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Db 661 GCGCGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Oy 944 TTGAGCAGTGTGACAAAAGATTAAGAGAGCTTTGGCTATGCTGCTGCTGCTGCTG 1003
Db 721 CTAAAGAGTGTGATGAGAAAGATTAAGAGAGAGCTGCTGCTGCTGCTGCTGCTG 780
Oy 1004 TCAAGAGATCTATTAAGTT-TGCTCATTTACATGTCGAAACCTGGA 1054
Db 781 TCAAGAGAGCTCTATTAAGTTCAAGCATCATCACTGTCACAAACCCAA 832

RESULT 11
AAH44261
ID AAH44261 standard; DNA; 1862 BP.
AC AAH44261;
XX
XX 21-SEP-2001 (first entry)
DE Physcomitrella patens 78_ppprot1_087_e12-259rev gene.
XX
XX Tocopherol and carotenoid metabolism related protein; TCMP; synthesis;
KW Physcomitrella patens; moss; algae; microorganism; fungus; plant;
KW identification; genome mapping; modulation; evolutionary study;
KW cellular production; fine chemical; ds.
XX
OS Physcomitrella patens.
PN WO200144276-A2.
XX
XX 21-JUN-2001.
PD
XX 14-DEC-2000; 2000MO-EPI2698.
PF
XX 16-DEC-1999; 99US-0171121.
PR
XX (BADI) BASF PLANT SCI GMBH.
PA

XX
PI Lerchl J, Renz A, Ehrhardt T, Reindl A, Cirpus P, Bischoff F;
PI Frank M, Freund A, Duwenig E, Schmidt R, Reski R, Badur R;
DR WPI: 2001-398121/42.
DR P-PSDB; AAB99888.
PT Tocopherol and carotenoid metabolism related protein (TCMP), used to
PT produce fine chemicals, is isolated from mosses, algae, microorganisms,
PT fungi, plants, or their fragments
PS Claim 6; Page 111-112; 123pp; English.
XX
XX The present invention describes isolated tocopherol and carotenoid
CC metabolism related proteins (TCMP) (1) from mosses or algae,
CC microorganisms or fungi, plants, or its fragments. (1) can be used as
CC enzymes in the production of fine chemicals or in the metabolism of
CC tocopherols and carotenoids. (1) also assist in transmembrane transport.
CC The fine chemicals that can be produced include lipids, fatty acids,
CC vitamins, cofactors, enzymes, amino acids, and nucleotide bases.
CC Nucleotide sequences, proteins, vectors and host cells from the present
CC invention can be used: (a) to identify mosses related to Physcomitrella
CC patens; (b) in mapping genomes of mosses related to Physcomitrella
CC patens; (c) in the modulation of TCMP activity; (d) in evolutionary
CC studies; (e) in the determination of functional TCMP regions; (f) and
CC in the cellular production of fine chemicals. AAH44222 to AAH44262
CC encode the Physcomitrella patens TCMP proteins given in AAB99849 to
CC AAB99889. AAH44212 to AAH44221 represent nucleotide sequence used in
CC the exemplification of the present invention.
XX
SQ Sequence 1862 BP; 465 A; 408 C; 521 G; 468 T; 0 other:
Query Match 27.1%; Score 322.2; DB 22; Length 1862;
Best Local Similarity 61.4%; Pred. No. 8; 8e-78;
Matches 541; Conservative 0; Mismatches 328; Indels 12; Gaps 1;
Oy 189 AGAAGAGCTGCGAAGGAGATGCGAGATTTTACGACAGTGTCTGCTTATGGGAGA 248
Db 377 AGCGGAGCTTTTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 436
Oy 249 ACATTTGGGGGCGACCATGACCATGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 296
Db 437 GCATTTGGGGGCGACCATGACCATGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 496
Oy 297 CTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 356
Db 497 TTGACGGGCGATCTGACACACCGGCGAGCGCAATCAAGATGATGAATCTCTGGCT 556
Oy 357 TTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 416
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Oy 417 GCATAGTGGAGCTGATAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 476
Db 617 GATAGGGGGAAGCTACGTTACTTGGCCCGGAAATTTCCAGGCGCAAGTGAATCCATCA 676
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Oy 717 ATCTTGCGCTGACGAACAATCTTATCTACATGAGGAGCAAGATCTTAAAGAGATT 776

| Db | Accession | Gene | Protein | Enzyme | Inhibitor | Herbicide |
|-----------|-----------|--------------------------------------------------------------------------|---------|--------|-----------|-----------|
| Db | 917 | ATCCGAGCCCGGTGAAACTTCTCTCAGACGAGAGATCTTTGGACAAAGATT | 976 | | | |
| QY | 777 | GCATGCGATTAATACCTCCCTGCTGCTCAACTTGTATTATGTTAAGTTGCTCCAT | 836 | | | |
| Db | 977 | GTAAGCGATTCATCTTGCCAGCGCTGGTGTCTCCCGCGAGACTACGCTCCATAGCCAAAG | 1036 | | | |
| QY | 837 | CCCTGTCACCTTCAGGACATCAGTCAGAAAGATTGGTCTCTGCTTTTGTCTCCATTTGGC | 896 | | | |
| Db | 1037 | ACTTAGCGCTCGACATCAAGAGGAGGGCTGTCGAGTAGCTGACGGCCCTCTGGC | 1096 | | | |
| QY | 897 | CAGCAGTAGATAGCCTCAGCGCTTCCATCAGAGGAGGCTATCTTCACTCTTGACAGCTGAC | 956 | | | |
| Db | 1097 | CAGGCGGATGAAACACCGCTTCTCCATGGAAGGCTGGTGGGACTGCTGCAAGTCCGGCT | 1156 | | | |
| QY | 957 | AAAAACGATAAAGAGAGCTTTGGCTATGCTCATGATAGTAGAGGATACAGAAAGATC | 1016 | | | |
| Db | 1157 | GGACTACTATGAAAGAGGCTTTCGCATGACGCTCATGATCAGAGGCTACACGAGGAGC | 1216 | | | |
| QY | 1017 | TAAATTAAGTTTCCCATCATTACATGTTCGAAACCTGAATTA | 1057 | | | |
| Db | 1217 | TCATTAATTCGCTGCATCATTGCGAAGGAGGATTGA | 1257 | | | |
| RESULT 12 | | | | | | |
| ID | AAA29151 | AAA29151 standard; cDNA; 792 BP. | | | | |
| XX | AC | AAA29151: | | | | |
| XX | DT | 12-SEP-2000 (first entry) | | | | |
| XX | DE | Corn gamma tocopherol methyltransferase partial coding sequence. | | | | |
| XX | KW | Vitamin E: alpha-tocopherol; biosynthesis; enzyme; inhibitor; herbicide; | | | | |
| XX | KM | gamma-tocopherol methyltransferase; ss. | | | | |
| XX | OS | Zea mays. | | | | |
| XX | FM | Key Location/Qualifiers | | | | |
| XX | FT | CDS 2..574 | | | | |
| XX | FT | /tag- a | | | | |
| XX | FT | /product- gamma_tocopherol_methyltransferase | | | | |
| XX | FT | /partial | | | | |
| XX | PM | WO200032757-A2. | | | | |
| XX | PD | 08-JUN-2000. | | | | |
| XX | PF | 02-DEC-1999; 99WO-0528568. | | | | |
| XX | PR | 03-DEC-1998; 98US-0110781. | | | | |
| XX | PA | (DUBO) DU PONT DE NEMOURS & CO E.I. | | | | |
| XX | PI | Cahoon RE, Coughlan SJ, Miao G, Rafalski JA; | | | | |
| XX | DR | WPI: 2000-412309/35. | | | | |
| XX | PS | P-PSDB: AAY96459. | | | | |
| XX | XX | Polynucleotide encoding a vitamin E biosynthetic enzyme polypeptide | | | | |
| XX | XX | such as gamma tocopherol methyltransferase, useful for synthesizing | | | | |
| XX | XX | vitamin E or as a target for design and discovery of herbicides | | | | |
| XX | XX | Claim 3: Page 49; 82pp; English. | | | | |
| XX | XX | AAA29151-69 encode vitamin E (alpha-tocopherol) biosynthetic enzymes or | | | | |
| XX | XX | their fragments. The cDNA clones were identified by BLAST searches based | | | | |
| XX | XX | on similarity to Synecocystis sp. and Arabidopsis thaliana vitamin E | | | | |
| XX | XX | biosynthetic enzymes. The enzymes are useful for synthesizing | | | | |
| XX | XX | plastoquinones or tocopherols (especially vitamin E). Vitamin E is | | | | |
| XX | XX | required for plant growth, therefore the enzymes may be used for the | | | | |
| XX | XX | discovery of new herbicides. The enzymes can be used in methods to | | | | |

| Query Match | 26.1% | Score 310: | DB 21: | Length 792: |
|-----------------------------------------------------------------------------|----------------------|--------------------|-----------------|-------------------|
| Best Local Similarity | 70.2% | Pred. No. 1.3e-74: | | |
| Matches 415: | Conservative | 0: | Mismatches 176: | Indels 0: Gaps 0: |
| CC evaluate potential inhibitors, which may have use as herbicides. | | | | |
| CC Additionally, transgenic expression of, e.g. gamma-tocopherol | | | | |
| CC methyltransferase affords the ability to manipulate tocopherol levels as | | | | |
| CC desired for a particular application. | | | | |
| XX | | | | |
| XX Sequence 792 BP: 201 A; 204 C; 215 G; 166 T; 6 other: | | | | |
| So | | | | |
| Qy 480 TGAGTCCGTGTTCAACGCTCAAGAGCAAGCAATGCTCTTGTGCTGCTGCTCAAGAGATTTGGCTGATA | | | | |
| Db 3 TGAGCCCTGTTTCAACCCGAGAGAGAAATGCTCTGCTGCTGAGACCGAGGGGTTGTGCGATC | | | | |
| Qy 540 AGGTTTCCCTTCAGGTGCTGACGCTTACACAGCAACCATTTCTCTGACGGCCAGTTTGATC | | | | |
| Db 63 AGGTTACTCTGCAATGCTGATCTGTGCTGAGCAACCGTTTCTGACGGGCGAGTTGCAATC | | | | |
| Qy 600 TGGTGTGGTCCATGAGAGAGTGGAGCAATGCTCCGACAGCAACAGCTTAAGTTTGTGGAGAT | | | | |
| Db 123 TGGTGTGGTCCATGAGAGATGGCGAGCATCCCGACAGAGAAAGTTTGTATGAGAC | | | | |
| Qy 660 TAGCTGGGGTACACAGACAGAGTGGCATTAATAATAGTAAATGATGCTGCCACAGGATC | | | | |
| Db 183 TAGCACCGCTGGCGGCTCTGTGAGGAGACATATATCATGCTGACATAGGTGCTCATAGAAC | | | | |
| Qy 720 TTGGCCCTGAGCAGCAATCTTTACATCCATGSGAGCAGATCTCTTAAGAAAGATTTGGG | | | | |
| Db 243 TGGATCCATCCGAAACCTCGCTAAAGCCCGATGAAGCTGAGCCTCCGAGAGGATATGCG | | | | |
| Qy 780 ATGCATATTACCTCCCTGCTGCTGCTGCTCAACTTCGATATATGTTAGTTGGTCCATGCC | | | | |
| Db 303 AGCGATACCTACCTCCCGGAGCTGGCTCACTTCACTTCACTATGGAACATTTGCCAATCAC | | | | |
| Qy 840 TGTCACTTACGAGCATCAAGTCAAGATTTGGTCTGCTTGTGCTCCATTTTGGCCAG | | | | |
| Db 363 TGTCTCTCGAGGATATCAAGACAGCTGACTGTGCGGAGAAACGTCGCCGTTTGGCCCG | | | | |
| Qy 900 CAGTGTACGCTCAGGCTTTCACATGAGAGGGTCTATCTTCACTCTTGAGCAGTGGACAA | | | | |
| Db 423 CGGTGTAATAATATCAGGCTTACATGAGAGGGCTTCACCTCTGCTGAGACACCGGATGG | | | | |
| Qy 960 AANCGATAAAGAGAGCTTTGGCTATGCCATTTGATGATAGAGGATTAAGAAAGATCTTA | | | | |
| Db 483 AGACGATCAAGAGCGGAGTGTGATCCCGCTAATGATCCAGGCTTACAGAGGGGCTCA | | | | |
| Qy 1020 TTAAGTTTGGCATTTACATGTCGAAAACTGAAATAAATGAGAGGCGAGC | | | | |
| Db 543 TCAAAATTCACATCATCACCCTGTGCGAAGGCTGGACCGCGTANAGAGAGAG | | | | |
| RESULT 13 | | | | |
| AX17788 | | | | |
| ID AX17788 standard; DNA; 954 BP. | | | | |
| XX AX17788: | | | | |
| XX 21-MAY-1999 (first entry) | | | | |
| XX Synecocystis gamma-tocopherol methyltransferase encoding gene. | | | | |
| De Synecocystis gamma-tocopherol methyltransferase encoding gene. | | | | |
| KW Gamma-tocopherol methyltransferase; gamma-TM; SLR0089; 165H57; meat; | | | | |
| KX transgenic plant; alpha-tocopherol; gamma-tocopherol; forage plant; ds. | | | | |
| OS Synecocystis sp. | | | | |
| OS | | | | |
| EH Key | Location/Qualifiers | | | |
| FT CDS | 1..954 | | | |
| FT | /+tag- a | | | |
| FT | /gene= "SLR0089" | | | |
| FT | /product= "gamma-TM" | | | |
| XX | | | | |

PN WO9094622-A1.
 XX
 PD 04-FEB-1999.
 XX
 PF 22-JUL-1998: 98WO-US15137.
 XX
 PR 17-JUL-1998: 98US-0053819.
 PR 25-JUL-1997: 97US-0053819.
 PR 26-JAN-1998: 98US-0072497.
 XX
 PA (UYNE-) UNIV NEVADA.
 XX
 PI Dellapenna D, Shintani DK;
 DR MPI: 1999-142458/12.
 DR P-PSDB: AAM95016.
 XX
 PT Newly isolated DNA fragment comprising a ^c-tocopherol (vitamin E)
 PT methyltransferase coding sequence - useful for producing
 PT ^a-tocopherol, and transgenic plants, seeds and oils with an altered
 PT tocopherol profile
 PS
 PS Claim 2: Page 33-35; 46pp; English.
 XX
 CC The invention provides DNA sequences encoding gamma-tocopherol
 CC methyltransferases (gamma-TMT). The gamma-TMT encoding genes SLR0089
 CC and 16H57 are isolated from Synchocystis and Arabidopsis species
 CC respectively. The DNA fragments are useful for producing transgenic
 CC plants containing a higher alpha-tocopherol:gamma-tocopherol ratio. They
 CC are also useful for producing alpha-tocopherol and plants with increased
 CC gamma-tocopherol, which may be useful in certain industries such as the
 CC meat industry e.g. for developing forage plants to feed animals. The
 CC production of transgenic plants (and seeds) with a higher alpha-
 CC tocopherol:gamma-tocopherol ratio, using the gamma TMTs, will increase
 CC the level of alpha-tocopherol in the human diet, in addition to enhancing
 CC the stability and shelf life of plants and plant products. Increased
 CC levels of alpha-tocopherol will also increase meat quality and extend
 CC shelf life of post-processed meat products. Plants with a higher alpha-
 CC tocopherol:gamma-tocopherol ratio may also produce advantageous
 CC phenotypes. The present sequence represents the SLR0089 gene encoding a
 CC Synchocystis gamma-TMT.
 CC
 XX
 SO Sequence 954 BP; 204 A; 232 C; 271 G; 247 T; 0 other;
 Query Match 12.4%; Score 147; DB 20; Length 954;
 Best Local Similarity 49.9%; Pred. No. 6e-30; Mismatches 420; Indels 9; Gaps 2;
 Matches 428; Conservative 0;

Db 449 TGGCAATGCGCTTGGATTGGCTTCTTCCTCCGATTCCTTGGACTGGGTTGGTCGTGG 508
 Qy 615 AGAGTGGAGACATATGCTGACAAAGCTAAGTTGTTGGAGTATGCTGGGTTACGAC 674
 Db 509 AAGTGGGGAGACATGCTCCCAACAAAGCTAGTTTACAGAAAGCTTGGGGGTACTTGA 568
 Qy 675 CACCAAGTGGCATTATATATAGTAACATGATGCGCACAGGAGATCTTGGCCCTGACGAAC 734
 Db 569 AACCAAGTGGCCGCTCATTTTACGACATGCTGCTACATGCTCCATGATGATCCGCGCAATG 628
 Qy 735 AATCCTTACATCCATGAGGACCAAGATCTTTAAAGAAATTTGGATGATATTAATCCTCC 794
 Db 629 GCCCCTGACTGCGATGAAAGCTGCGCATCTCCAAAGCATCTATGACGTTTACTGTTGC 688
 Qy 795 CTGCTGTGCTCAACTTGTGATATATATATGTTGCTCCATCCCTCTCCTCAGACACA 854
 Db 689 CCTATGCTGTTTCCCTGCGGACTACGAGCGATCCGAGGAATGTTGGGTGGGAAA 748
 Qy 855 TCAAGTCAGAAAGATGCTGCTGCTTGTGCTCCATTTTGGCCAGCAGTATAGCTCAG 914
 Db 749 TTAAGACTGCGGATGTTGTCAGTGCGGTGACCTTTTGGACCGGCTGATGAGCTCG 808
 Qy 915 CTTTACATGGAAGGCTCTATCTTCTTCACTCTTGAACAGTGACAAAAACGATAAAGAG 974
 Db 809 CGTTGCAATCCCGGGGTTGTGGCCCTTGGGGCAAGCGGGCCAAAAATATCAATGCCG 868
 Qy 975 CTTTGGCTATGCTATGATGATGAGGATGATCAAGAAAGCTATTAATTAATTTGCCATCA 1034
 Db 869 CCTGTGTTTACATTAATTAATTAATGAGGCTATGACGAGGATTAATGCTGTTGGCTTAT 928
 Qy 1035 TTACATGTCGAAAACCT 1051
 Db 929 TTAAGGGGATTAAGCCT 945
 RESULT 14
 ID AAA29152 standard; CDNA: 521 BP.
 AC AAA29152;
 XX
 DT 12-SEP-2000 (first entry)
 XX
 DE Partial gamma tocopherol methyltransferase cDNA, clone r10n.pK085.e11.
 XX
 KW Vitamin E; alpha-tocopherol; biosynthesis; enzyme; inhibitor; herbicide;
 KW gamma-tocopherol methyltransferase; ss.
 OS Oryza sativa.
 XX
 FH Key Location/Qualifiers
 FT 1.246 /tag= a
 FT /product= gamma_tocopherol_methyltransferase
 FT /partial
 PM WO200032757-A2.
 XX
 PD 08-JUN-2000.
 XX
 PF 02-DEC-1999: 99WO-US28588.
 XX
 PR 03-DEC-1998: 98US-0110781.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Cahoon RE, Coughlan SJ, Miao G, Rafalski JA;
 XX
 DR MPI: 2000-412309/35.
 DR P-PSDB: AAY96460.
 XX
 PT Polynucleotide encoding a vitamin E biosynthetic enzyme polypeptide

PT such as gamma tocopherol methyltransferase, useful for synthesizing
PT vitamin E or as a target for design and discovery of herbicides

PS Claim 3; Page 50; 82pp; English.

CC AAA29151-69 encode vitamin E (alpha-tocopherol) biosynthetic enzymes or
CC their fragments. The cDNA clones were identified by BLAST searches based
CC on similarity to Synecocystis sp. and Arabidopsis thaliana vitamin E
CC biosynthetic enzymes. The enzymes are useful for synthesizing
CC plastoquinones or tocopherols (especially vitamin E). Vitamin E is
CC required for plant growth, therefore the enzymes may be used for the
CC discovery of new herbicides. The enzymes can be used in methods to
CC evaluate potential inhibitors, which may have use as herbicides.
CC Additionally, transgenic expression of, e.g. gamma-tocopherol
CC methyltransferase affords the ability to manipulate tocopherol levels as
CC desired for a particular application.

XX Sequence 521 BP; 156 A; 114 C; 119 G; 116 T; 16 other;

SO Query Match 10.6%; Score 125.8; DB 21; Length 521;

Best Local Similarity 70.1%; Pred. No. 2.9e-24; Indels 0; Gaps 0;

Matches 169; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

OY 633 CTGCAAAAGCTAGTTGTTGGAGAGTTAGCTCGGTAGCAGCACCAGTGCATTATTA 692

DB 5 CAGACAAAGCGAGTTGTGTAAGCAGCTGCAGCGCTCCGAGCGGCGAGATAA 64

OY 693 TAATAGTACATGCTGCCACAGGATCTTGCCCTGACGAAACAATCTTACATCAGGG 752

DB 65 TCATTGTGACCTGCTGCATAGGAACTCCAGCCATCCGAAGAGTCCCTGAACCTGANTG 124

OY 753 AGCAAGATCTCTTAAAGAGATTGGATGATATTAACCTCCGCTGGTGCCTCACTT 812

DB 125 AGCTGAATCTCTGAAAGATATGCGATGATATTAATCTCCAGACTGGTCTCTCTT 184

OY 813 CTGATTATGTTAAGTTGCTCCAAATCCCTGTCACCTTCAGGACATCAAGTCAGAAATTGGT 872

DB 185 CTGATTATGTCAAAATTGCCGAGTCACATGCTCTTGAAGATATTAAGACACACTGATTGGT 244

OY 873 C 873

DB 245 C 245

RESULT 15

ID AAA29162 standard; cDNA; 521 BP.

XX AAA29162;

DT 12-SEP-2000 (first entry)

DE Rice gamma-tocopherol methyltransferase cDNA clone rls72.pk0010.g3-3'

KW Vitamin E; alpha-tocopherol; biosynthesis; enzyme; inhibitor; herbicide;

KM gamma-tocopherol methyltransferase; ss.

OS Oryza sativa.

PN MO200032757-A2.

PD 08-JUN-2000.

PE 02-DEC-1999; 99WO-US28588.

PR 03-DEC-1998; 98US-0110781.

PA (DUPO) DU PONT DE NEMOURS & CO E I.

PI Cahoon RE, Coughlan SJ, Miao G, Rafalski JA;

DR WPI; 2000-412309/35.

PT Polynucleotide encoding a vitamin E biosynthetic enzyme polypeptide
PT such as gamma tocopherol methyltransferase, useful for synthesizing
PT vitamin E or as a target for design and discovery of herbicides

PS Claim 3; Page 63; 82pp; English.

CC AAA29151-69 encode vitamin E (alpha-tocopherol) biosynthetic enzymes or
CC their fragments. The cDNA clones were identified by BLAST searches based
CC on similarity to Synecocystis sp. and Arabidopsis thaliana vitamin E
CC biosynthetic enzymes. The enzymes are useful for synthesizing
CC plastoquinones or tocopherols (especially vitamin E). Vitamin E is
CC required for plant growth, therefore the enzymes may be used for the
CC discovery of new herbicides. The enzymes can be used in methods to
CC evaluate potential inhibitors, which may have use as herbicides.
CC Additionally, transgenic expression of, e.g. gamma-tocopherol
CC methyltransferase affords the ability to manipulate tocopherol levels as
CC desired for a particular application.
CC Note: The specification indicates that this sequence should encode the
CC protein given in AAY96470.

XX Sequence 521 BP; 156 A; 114 C; 119 G; 116 T; 16 other;

SO Query Match 10.6%; Score 125.8; DB 21; Length 521;

Best Local Similarity 70.1%; Pred. No. 2.9e-24; Indels 0; Gaps 0;

Matches 169; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

OY 633 CTGCAAAAGCTAGTTGTTGGAGAGTTAGCTCGGTAGCAGCACCAGTGCATTATTA 692

DB 5 CAGACAAAGCGAGTTGTGTAAGCAGCTGCAGCGCTCCGAGCGGCGAGATAA 64

OY 693 TAATAGTACATGCTGCCACAGGATCTTGCCCTGACGAAACAATCTTACATCAGGG 752

DB 65 TCATTGTGACCTGCTGCATAGGAACTCCAGCCATCCGAAGAGTCCCTGAACCTGANTG 124

OY 753 AGCAAGATCTCTTAAAGAGATTGGATGATATTAACCTCCGCTGGTGCCTCACTT 812

DB 125 AGCTGAATCTCTGAAAGATATGCGATGATATTAATCTCCAGACTGGTCTCTCTT 184

OY 813 CTGATTATGTTAAGTTGCTCCAAATCCCTGTCACCTTCAGGACATCAAGTCAGAAATTGGT 872

DB 185 CTGATTATGTCAAAATTGCCGAGTCACATGCTCTTGAAGATATTAAGACACACTGATTGGT 244

OY 873 C 873

DB 245 C 245

Search completed: March 18, 2003, 07:21:16
Job time : 1536 secs

GenCore version 5.1.4 p5.4578
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OM nucleic - nucleic search, using sw model

Run on: March 18, 2003, 06:53:09 ; Search time 294 Seconds
(without alignments)
1240.268 Million cell updates/sec

Title: US-09-857-613A-27

Perfect score: 1189
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents-NA: *
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3: /cgn2_6/ptodata/1/ina/6A.COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PTCUTS.COMB.seq: *
6: /cgn2_6/ptodata/1/ina/Backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------------------|----------------------|
| 1 | 76.6 | 6.4 | 957 | US-09-382-906A-1 | Sequence 1, Appl 1 |
| 2 | 51 | 4.3 | 7218 | US-08-232-463-14 | Sequence 14, Appl 1 |
| 3 | 42.4 | 3.6 | 1400 | US-09-041-718-1 | Sequence 1, Appl 1 |
| 4 | 40.6 | 3.4 | 436 | US-09-397-787-257 | Sequence 257, Appl 1 |
| 5 | 40.2 | 3.4 | 1447 | US-09-443-041A-27 | Sequence 27, Appl 1 |
| 6 | 39.4 | 3.3 | 3157 | 5198347-3 | Patent No. 5198347 |
| 7 | 38.8 | 3.3 | 1508 | US-09-039-046-1 | Sequence 1, Appl 1 |
| 8 | 38.8 | 3.3 | 2706 | US-09-463-238-2 | Sequence 2, Appl 1 |
| 9 | 38.8 | 3.3 | 2806 | US-09-463-238-11 | Sequence 11, Appl 1 |
| 10 | 38.2 | 3.2 | 1736 | US-09-182-816-24 | Sequence 22, Appl 1 |
| 11 | 38.2 | 3.2 | 1736 | US-09-471-528-22 | Sequence 22, Appl 1 |
| 12 | 38.2 | 3.2 | 1736 | US-09-471-528-22 | Sequence 22, Appl 1 |
| 13 | 38.2 | 3.2 | 1736 | US-09-471-528-22 | Sequence 22, Appl 1 |
| 14 | 38.2 | 3.2 | 1736 | US-09-634-530-24 | Sequence 24, Appl 1 |
| 15 | 38.2 | 3.2 | 1736 | US-09-634-530-24 | Sequence 24, Appl 1 |
| 16 | 37.8 | 3.2 | 1558 | US-08-455-550-7 | Sequence 7, Appl 1 |
| 17 | 37.8 | 3.2 | 3080 | US-09-099-041A-25 | Sequence 25, Appl 1 |
| 18 | 37.8 | 3.2 | 3080 | US-09-245-281-25 | Sequence 25, Appl 1 |
| 19 | 37.8 | 3.2 | 3080 | US-09-207-359B-25 | Sequence 25, Appl 1 |
| 20 | 37.8 | 3.2 | 6200 | US-09-439-923-1 | Sequence 13, Appl 1 |
| 21 | 37.8 | 3.2 | 19124 | US-08-487-826B-13 | Sequence 13, Appl 1 |
| 22 | 37.6 | 3.2 | 3138 | US-07-867-106-4 | Sequence 4, Appl 1 |
| 23 | 37.4 | 3.1 | 1332 | US-09-412-600B-1 | Sequence 1, Appl 1 |
| 24 | 37.4 | 3.1 | 7941 | US-09-816-703A-1 | Sequence 1, Appl 1 |
| 25 | 37 | 3.1 | 289 | US-09-007-005-17 | Sequence 17, Appl 1 |
| 26 | 37 | 3.1 | 289 | US-09-244-796-17 | Sequence 17, Appl 1 |
| 27 | 37 | 3.1 | 1986 | US-08-687-590-57 | Sequence 57, Appl 1 |

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| c | 28 | 37 | 3.1 | 5852 | 1 | US-07-867-106-2 | Sequence 2, Appl 1 |
| | 29 | 36.8 | 3.1 | 1123 | 4 | US-09-152-060-15 | Sequence 15, Appl 1 |
| | 30 | 36.8 | 3.1 | 1210 | 4 | US-09-443-041A-29 | Sequence 29, Appl 1 |
| | 31 | 36.8 | 3.1 | 2280 | 1 | US-08-813-150-1 | Sequence 1, Appl 1 |
| | 32 | 36.8 | 3.1 | 3792 | 2 | US-08-992-334-1 | Sequence 1, Appl 1 |
| | 33 | 36.8 | 3.1 | 3792 | 3 | US-08-302-752-1 | Sequence 1, Appl 1 |
| | 34 | 36.8 | 3.1 | 5234 | 2 | US-08-992-334-2 | Sequence 2, Appl 1 |
| | 35 | 36.8 | 3.1 | 5234 | 3 | US-08-302-752-3 | Sequence 3, Appl 1 |
| | 36 | 36.8 | 3.1 | 6722 | 2 | US-08-992-334-3 | Sequence 3, Appl 1 |
| | 37 | 36.8 | 3.1 | 6722 | 3 | US-08-302-752-3 | Sequence 3, Appl 1 |
| | 38 | 36.4 | 3.1 | 144 | 1 | US-08-702-344-26 | Sequence 26, Appl 1 |
| | 39 | 36.4 | 3.1 | 1104 | 4 | US-09-009-816-1 | Sequence 9, Appl 1 |
| | 40 | 36.4 | 3.1 | 1172 | 1 | US-07-945-288-9 | Sequence 9, Appl 1 |
| | 41 | 36.4 | 3.1 | 1172 | 1 | US-08-462-831-9 | Sequence 9, Appl 1 |
| | 42 | 36.4 | 3.1 | 1172 | 1 | US-08-461-809-9 | Sequence 9, Appl 1 |
| | 43 | 36.4 | 3.1 | 1172 | 1 | US-08-461-441-9 | Sequence 9, Appl 1 |
| | 44 | 36.4 | 3.1 | 1172 | 5 | PCR-US93-08518-9 | Sequence 9, Appl 1 |
| | 45 | 36.2 | 3.0 | 1622 | 2 | US-09-014-969-16 | Sequence 16, Appl 1 |

ALIGNMENTS

RESULT 1
US-09-382-906A-1
; Sequence 1, Application US/09382906A
; Patent No. 6448475
; GENERAL INFORMATION:
; APPLICANT: Dellepenna, Dean
; APPLICANT: Shintani, David
; TITLE OF INVENTION: Manipulation of Tocopherol Levels in Transgenic Plants
; FILE REFERENCE: 920905, 90032
; CURRENT APPLICATION NUMBER: US/09/382, 906A
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 60/097, 863
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 957
; TYPE: DNA
; ORGANISM: Synechocystis PCC6803
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(954)
US-09-382-906A-1

Query Match 6.4%; Score 76.6; DB 4; Length 957;
Best Local Similarity 54.7%; Pred. No. 3e-12;
Matches 179; Conservative 0; Mismatches 139; Indels 9; Gaps 1;

| | | | |
|----|-----|-----------------------------------------------------------|-----|
| QY | 399 | TACTGATGTTGGGTGGGATAGTGGCATCTAGATCGGCGCAAGAAATTTGAG | 458 |
| DB | 290 | TATTTGATGTTGGGTGGGATAGTGGCATCTAGATCGGCGCAAGAAATTTGAG | 349 |
| QY | 459 | CAACACGTAGTACGATCTGAGTCTTCAAGTCAAGACAAATGCTTCTG | 518 |
| DB | 350 | TTACGTATACCGGATGATCCATGATCCCAAGAGTGAACGGGCGACGAAATTAATC | 409 |
| QY | 519 | CTGCTCAAGATGTTGCTGATRAAGTTCCTTTTCAGGTTGCTGACGCTTACAGAACAT | 578 |
| DB | 410 | CTCCGAGTGTGACGCGCCAG-----TTTGGGTTGAGAGATGCTATGCTTGTCTT | 460 |
| QY | 579 | TCTCTGAGCGGCGGATTTGATCTGTTGTCATGAGAGTGAAGATGCTGAC | 638 |
| DB | 461 | TTCTGAGCGGATTTGATCTGTTGTCATGAGAGTGAAGATGCTGAC | 520 |
| QY | 639 | AAGCTAAGTTTGTGAGAGTTTACCTCGGTAGGACGACGATGCTATTAATTAATAG | 698 |
| DB | 521 | AAGCTGTTTGTGAGAGTTTACCTCGGTAGGACGACGATGCTATTAATTAATAG | 580 |
| QY | 699 | TAACTGTGCTCCACAGGATTTGCTG | 725 |

DB 581 CGGATTGCAATCAGCGGACGATCGCC 607

RESULT 2

US-08-232-463-14/C
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEFFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0239
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PT2gpt-F1s
US-08-232-463-14

Query Match 4.3%; Score 51; DB 1; Length 7218;
Best Local Similarity 12.4%; Pred. No. 0.0015;
Matches 45; Conservative 164; Mismatches 154; Indels 0; Gaps 0;

OY 827 TTGTCACATCCCTGCTTCTGAGCATCAGTCAGAGATGGCTGCTTGTGCT 886
DB 1535 TCGCTTACAGCGCATCTATGTTCAAAAAGCGATGAGCATCTAGTAATTTAC 1476
OY 887 CCATTTGGCCAGCAGTATACGCTTCACATGGAAGGCTATCTTACACTTG 946
DB 1475 CTATCTAGCAGAGTAAAGAGATGAGAATTTGCTACRRRRRRRRRRRRR 1416
OY 947 AGCATGCAAAAAACATAAAGAGCTTTGCTATGCCATTTGATGATAGAGGATAC 1006
DB 1415 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1356
OY 1007 AAGAAGATCTAATTAAGTTTCCATCTTACATGTCGAAACCGAATAAATGGAGAG 1066
DB 1355 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1296
OY 1067 CAGGATTAATTAATGAGTAACCAAGTTTCAACAGGTCTTATTTGATAGTTGAG 1126

DB 1295 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1236

OY 1127 AAACAGAGAAAAATTAATGAAGGGCTTTCGATTTTAAAAA 1186

DB 1235 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1176

OY 1187 AAA 1189

DB 1175 RRR 1173

RESULT 3

US-09-041-718-1
Sequence 1, Application US/09041718A
Patent No. 6225075
GENERAL INFORMATION:
APPLICANT: Baird, Martin
TITLE OF INVENTION: DNA encoding sterol methyltransferase
FILE REFERENCE: 740 003051
CURRENT APPLICATION NUMBER: US/09/041,718A
CURRENT FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1400
TYPE: DNA
ORGANISM: Candida albicans
US-09-041-718-1

Query Match 3.6%; Score 42.4; DB 4; Length 1400;
Best Local Similarity 46.3%; Pred. No. 0.019;
Matches 139; Conservative 0; Mismatches 161; Indels 0; Gaps 0;

OY 391 CAAGATATAGTATGATGTTGGTGTGAGTGCAGCTAGATACCTGGCCAAAGAA 450
DB 507 CAGGAAGTTTATGATGTTGTTGTGTGTAGTGTGCTCCGTAGAGAAATCAAGATT 566
OY 451 ATTGAGCAACCGATGATGATGATGATGATGATGATGATGATGATGATGATG 510
DB 567 TACTGATTTGAAATTTGATGATTAATTAATTAATTAATTAATTAATTAATTA 626
OY 511 TCTTGTGCTGCTCAAGGATGATGATGATGATGATGATGATGATGATGATGATG 570
DB 627 TTAGCTAAAAAATACCATTTAGATCAATAATTAATTAATTAATTAATTAATTA 666
OY 571 GCACCATCTCTGACGGCCAGTTTGTATGCTGTGCTCCATGAGAGTGAAGATAT 630
DB 687 AATGATTTTGAACAGAAATCATTCATGCTGTTTATGCCATTTGAAGCTACCTTATGC 746
OY 631 GCCTGACAAAGCTAATGTTGTTGAGAGATTAGCTCGGTTAGCAGCACCAAGTCCATTAT 690
DB 747 TCCAGTTTGAAGAGATTATTCAGAAATTTAAAGTTTGAACCAAGTGTGATTTT 806
US-09-397-787-257
Sequence 257, Application US/09397787
Patent No. 6468758
GENERAL INFORMATION:
APPLICANT: Benson, Darin R.
APPLICANT: Lodes, Michael J.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR OVARIAN
FILE REFERENCE: 210121.466C2
CURRENT APPLICATION NUMBER: US/09/397,787
CURRENT FILING DATE: 1999-09-16
NUMBER OF SEQ ID NOS: 334
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 257
LENGTH: 436

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; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(436)
; OTHER INFORMATION: n = A,T,C or G
US-09-397-787-257
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Query Match
Best Local Similarity 3.4%; Score 40.6; DB 4; Length 436;
Matches 100; Conservative 0; Mismatches 100; Indels 0; Gaps 0;
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OY 30 CATCTCATGATCCACATCCACAGCTCCGTTCCCAATCCCTCCGACTTTCGCCAGAA 89
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DB 6 CACCCCTCCGCGCTCCAGGGCCCTCCGCTCCGCGCCCGGGACCCCGGCTCCCGCCAGCC 65
OY 90 TCCGGGTCCGACCCAGCTCTGGGCTCTTATTCGGGCATCGGACGAGCTCGAGAGAG 149
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 66 CCGGCCCGCGCCCGCCGACCATGTCTCATGATTAAGCTGTGAGGACGCGCGAGTTGAGCG 125
OY 150 GGGAGATGATTTGGAGAGAGCCGAGAGATGACAGAGATGACAGAGTGCAGAGAGGAA 209
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 126 CCAAGACCTGGAAGAGAGAGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAA 185
OY 210 TCGCAGAGTTTACGAGAGAG 229
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 186 AGAAGAGAGTGTGAGAGAG 205
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RESULT 5

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US-09-443-041A-27
; Sequence 27, Application US/09443041A
; Patent No. 6455717
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Orozco, Buddy
; APPLICANT: Rafalski, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Sterol Metabolism Enzymes
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/443,041A
; CURRENT FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: 60/109,283
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 27
; LENGTH: 1447
; TYPE: DNA
; ORGANISM: Glycine max
US-09-443-041A-27
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Query Match
Best Local Similarity 3.4%; Score 40.2; DB 4; Length 1447;
Matches 69; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
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OY 1073 TACTTTATGATGACCAAGTTCACAGCTGCTTATTCGATGATGAGAAAGAA 1132
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1229 TATGTTTATGAAATTAACCAACACTCTCTAAGGCTGTGTTGTTGTTAAAGAAAGA 1288
OY 1133 GAGAAATAATTAATGAAGAGGCTTTCGATTTTAAATAAAAAAAAAAAAAA 1189
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1289 TGGCAATGCAAGAGAAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1345
```

RESULT 6

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5198347-3
; Patent No. 5198347
; APPLICANT: Miller, Louis H.; Adams, John H.; Kaslow,
; DAVID C.; FANG, XIANGDOUG
; TITLE OF INVENTION: DNA ENCODING PLASMODIUM VIVAX AND
; PLASMODIUM KNOWLESII DUFFY RECEPTOR
; NUMBER OF SEQUENCES: 27
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/554,837
; FILING DATE: 20-JUL-1990
; SEQ ID NO:3
; LENGTH: 3157
5198347-3
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Query Match
Best Local Similarity 3.3%; Score 39.4; DB 6; Length 3157;
Matches 55; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
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```
OY 1109 TTTATTTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1168
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 3076 TATTTTCTATATGACAAATAAAAAAAAAAAAAAAAAAATACCATTTCAATATTTGA 3135
OY 1169 AAAAAAAAAAAAAAAAAA 1189
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DB 3136 AAAAAAAAAAAAAAAAAA 3156
```

RESULT 7

```
US-09-039-046-1
; Sequence 1, Application US/09039046
; Patent No. 6331660
; GENERAL INFORMATION:
; APPLICANT: CHOMET, PAUL S.
; APPLICANT: FREY, MONIKA
; APPLICANT: GIERL, ALFONS
; TITLE OF INVENTION: MAIZE DIMBOA BIOSYNTHESIS GENES
; FILE REFERENCE: DKM:131
; CURRENT APPLICATION NUMBER: US/09/039,046
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1508
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (49)..(1089)
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-09-039-046-1
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```
Query Match
Best Local Similarity 3.3%; Score 38.8; DB 4; Length 1508;
Matches 67; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
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```
OY 1076 TTTATGATGATGACCAAGTTCACAGCTGCTTATTCGATGATGAGAAAGAG 1135
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DB 1370 TCTGTGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1429
OY 1136 AAAAAAAAAATAAGAAAGGCTTTCGATTTTAAATAAAAAAAAAAAAAA 1189
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1430 AAAAAAAAAAAAAAAAAA 1483
```

RESULT 8

```
US-09-463-238-2
; Sequence 2, Application US/09463238
; Patent No. 6469230
; GENERAL INFORMATION:
; APPLICANT: Edwards, Elizabeth A
; APPLICANT: Smith, Alison M
; APPLICANT: Bustos Guillen, Regla
; APPLICANT: Martin, Catherine R
; APPLICANT: Plant Bioscience Limited
; TITLE OF INVENTION: Starch Debranching Enzymes
; FILE REFERENCE: 97.118
; CURRENT APPLICATION NUMBER: US/09/463,238
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: PCT/GB98/02280
```

;; PRIOR FILING DATE: 1998-07-30
;; PRIOR APPLICATION NUMBER: GB 9716185.5
;; PRIOR FILING DATE: 1997-07-31
;; NUMBER OF SEQ ID NOS: 30
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 2
;; LENGTH: 2706
;; TYPE: DNA
;; ORGANISM: Solanum tuberosum
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (2641)
;; OTHER INFORMATION: n = a or g or c or t
US-09-463-238-2

Query Match
Best Local Similarity 66.3%; Score 38.8; DB 4; Length 2706;
Matches 55; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

OY 1107 CGTTTATTCGATGAGTGGAGAACAGAGAAAAATTAATGAAGGGTTGTCGATTTT 1166
DB 2606 CTGTGATTTTAAATTCGATTTATTAATAAATTAATAGTGAATTCCTGTCGAAAAA 2665
OY 1167 AAAAAAAAAAAAAAAAAAAAAA 1189
DB 2666 AAAAAAAAAAAAAAAAAAAAAA 2688

RESULT 9

US-09-463-238-11
;; Sequence 11, Application US/09463238
;; Patent No. 6469230
;; GENERAL INFORMATION:
;; APPLICANT: Edwards, Elizabeth A
;; APPLICANT: Smith, Allison M
;; APPLICANT: Bustos Guillen, Regla
;; APPLICANT: Martin, Catherine R
;; APPLICANT: Plant Bioscience Limited
;; TITLE OF INVENTION: Starch Debranching Enzymes
;; FILE REFERENCE: 97.118
;; CURRENT APPLICATION NUMBER: US/09/463,238
;; CURRENT FILING DATE: 2000-01-21
;; PRIOR APPLICATION NUMBER: PCT/GB98/02280
;; PRIOR FILING DATE: 1998-07-30
;; PRIOR APPLICATION NUMBER: GB 9716185.5
;; PRIOR FILING DATE: 1997-07-31
;; NUMBER OF SEQ ID NOS: 30
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 11
;; LENGTH: 2806
;; TYPE: DNA
;; ORGANISM: Solanum tuberosum
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (826, 826, 2707 and 2797)
;; OTHER INFORMATION: n = a or g or c or t
US-09-463-238-11

Query Match
Best Local Similarity 66.3%; Score 38.8; DB 4; Length 2806;
Matches 55; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

OY 1107 CGTTTATTCGATGAGTGGAGAACAGAGAAAAATTAATGAAGGGTTGTCGATTTT 1166
DB 2672 CTGTGATTTTAAATTCGATTTATTAATAAATTAATAGTGAATTCCTGTCGAAAAA 2731
OY 1167 AAAAAAAAAAAAAAAAAAAAAA 1189
DB 2732 AAAAAAAAAAAAAAAAAAAAAA 2754

RESULT 10
US-09-182-816-22

;; Sequence 22, Application US/09182816
;; Patent No. 6143542
;; GENERAL INFORMATION:
;; APPLICANT: Wisniewski, Nancy
;; APPLICANT: Silver, Gary M.
;; APPLICANT: Lo, Katherine C.
;; APPLICANT: Brandt, Kevin S.
;; TITLE OF INVENTION: NOVEL FLEA EPOXIDE HYDROLASE NUCLEIC ACID MOLECULES,
;; TITLE OF INVENTION: PROTEINS AND USES THEREOF
;; FILE REFERENCE: FC-3-C1
;; CURRENT APPLICATION NUMBER: US/09/182,816
;; EARLIER APPLICATION NUMBER: 08/989,510
;; EARLIER FILING DATE: 1997-12-12
;; NUMBER OF SEQ ID NOS: 31
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 22
;; LENGTH: 1736
;; TYPE: DNA
;; ORGANISM: Ctenocephalides felis
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (159)..(1553)
US-09-182-816-22

Query Match
Best Local Similarity 50.3%; Score 38.2; DB 3; Length 1736;
Matches 94; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

OY 1003 ATACAGAGAAGATCTAATTAATTAAGTTGCCATCATTACATGCGAAACCTGAATAATGA 1062
DB 1538 AGAAGATAGAGATCTCGAAGAACTGTAAATTAATTCGATAAATAATATGTTAA 1597
OY 1063 GAGCAGCATTTACTTTATPAGAAATGACCAAGTTTCCACAGCGTTTATTCGATAGT 1122
DB 1598 AATTAATGTAAATTTACTGTGAATAACGATATGATTTTATTCACACTGTCAAATVAT 1657
OY 1123 TGAGAAACAGAGAAAAATTAATGAAGGGTTGTCGATTTTAAAAA 1182
DB 1658 AAAAAAAAAAAAAAAAAAAAAA 1717
OY 1183 AAAAAA 1189
DB 1718 AAAAAA 1724

RESULT 11

US-09-182-816-24/C
;; Sequence 24, Application US/09182816
;; Patent No. 6143542
;; GENERAL INFORMATION:
;; APPLICANT: Wisniewski, Nancy
;; APPLICANT: Silver, Gary M.
;; APPLICANT: Lo, Katherine C.
;; APPLICANT: Brandt, Kevin S.
;; TITLE OF INVENTION: NOVEL FLEA EPOXIDE HYDROLASE NUCLEIC ACID MOLECULES,
;; TITLE OF INVENTION: PROTEINS AND USES THEREOF
;; FILE REFERENCE: FC-3-C1
;; CURRENT APPLICATION NUMBER: US/09/182,816
;; EARLIER APPLICATION NUMBER: 08/989,510
;; EARLIER FILING DATE: 1997-12-12
;; NUMBER OF SEQ ID NOS: 31
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 24
;; LENGTH: 1736
;; TYPE: DNA
;; ORGANISM: Ctenocephalides felis
US-09-182-816-24

Query Match
Best Local Similarity 50.3%; Score 38.2; DB 3; Length 1736;
Matches 94; Conservative 0; Mismatches 93; Indels 0; Gaps 0;


```
OY 1003 ATACAGAAAGATCTAATTAGTTGCCATCATACATGCGAAACCTGATAATGGA 1062
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1538 AGAGAAATGAGATCTCTGAGAACTGTGATTAATTAATTGTGATTAATTAATGTTAA 1597
OY 1063 GAGCAGGATTTACTTTTATAGATGAACCAAGTTCCAAACAGTGTATTATTCGATAGT 1122
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1598 AAATAAATGTAATTAAGTGAATAAAGATGATTTTATTCAAACTGTCAATAT 1657
OY 1123 TGAGAAACAAGAGAAAAAATTAATGAAGGGGTTGTCGATTTTAAAAA 1182
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1658 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1717
OY 1183 AAAAAA 1189
      | | | | | | | |
Db 1718 AAAAAA 1724
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RESULT 15

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US-09-634-530-24/C
; Sequence 24, Application US/09634530
; Patent No. 6290958
; GENERAL INFORMATION:
; APPLICANT: Wisniewski, Nancy
; APPLICANT: Silver, Gary M.
; APPLICANT: Lo, Katherine C.
; APPLICANT: Brandt, Kevin S.
; TITLE OF INVENTION: FLEA EPOXIDE HYDROLASE PROTEINS AND USES THEREOF
; FILE REFERENCE: FC-3-CI-1
; CURRENT APPLICATION NUMBER: US/09/634,530
; CURRENT FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 09/471,528
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: 09/182,816
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 08/989,510
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentl Ver. 2.0
; SEQ ID NO 24
; LENGTH: 1736
; TYPE: DNA
; ORGANISM: Ctenocephalides felis
US-09-634-530-24
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Query Match 3.2%; Score 38.2; DB 4; Length 1736;
Best Local Similarity 50.3%; Pred. No. 0.33;

Matches 94; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

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Db 199 AGAGAAATGAGATCTCTGAGAACTGTGATTAATTAATTGTGATTAATTAATGTTAA 140
OY 1063 GAGCAGGATTTACTTTTATAGATGAACCAAGTTCCAAACAGTGTATTATTCGATAGT 1122
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 139 AAATAAATGTAATTAAGTGAATAAAGATGATTTTATTCAAACTGTCAATAT 80
OY 1123 TGAGAAACAAGAGAAAAAATTAATGAAGGGGTTGTCGATTTTAAAAA 1182
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 79 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 20
OY 1183 AAAAAA 1189
      | | | | | | | |
Db 19 AAAAAA 13
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Search completed: March 18, 2003, 11:33:02
Job time : 317 secs

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: March 18, 2003, 08:23:37 ; Search time 108 Seconds
(without alignments)
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Title: US-09-857-613a-27

Perfect score: 1189

Sequence: 1 ggacatggccaccctggtgta.....aaaaaaaaaaaaaaaa 1189

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 501302 seqs, 350932545 residues

Total number of hits satisfying chosen parameters: 1002604

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PC7_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PC7US_PUBCOMB.seq:*
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- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|---------------------|
| 1 | 194.4 | 16.3 | 252 | 10 | US-09-878-574-695 |
| 2 | 124.8 | 10.5 | 311 | 10 | US-09-294-0938-3472 |
| 3 | 44.6 | 3.8 | 286 | 10 | US-09-960-352-13342 |
| 4 | 43.6 | 3.7 | 2045 | 10 | US-09-925-300-749 |
| 5 | 42.6 | 3.6 | 932 | 12 | US-10-078-929-65 |
| 6 | 42.2 | 3.5 | 368 | 10 | US-09-834-975-47 |
| 7 | 42.2 | 3.5 | 2000 | 9 | US-09-938-842A-3589 |
| 8 | 41.8 | 3.5 | 401 | 10 | US-09-960-352-14060 |
| 9 | 41.6 | 3.5 | 1046 | 10 | US-09-925-297-307 |
| 10 | 41.4 | 3.5 | 393 | 10 | US-09-960-352-4582 |
| 11 | 41.2 | 3.5 | 620 | 10 | US-09-925-297-303 |
| 12 | 41.2 | 3.5 | 4840 | 10 | US-09-880-107-3423 |
| 13 | 41.1 | 3.4 | 347 | 10 | US-09-960-352-3371 |
| 14 | 41.1 | 3.4 | 419 | 10 | US-09-960-352-11234 |
| 15 | 41.1 | 3.4 | 2608 | 10 | US-09-739-254-16 |
| 16 | 41.1 | 3.4 | 2608 | 10 | US-09-904-615-16 |
| 17 | 40.8 | 3.4 | 1457 | 9 | US-09-989-920-93 |
| 18 | 40.6 | 3.4 | 436 | 10 | US-09-876-889-257 |
| 19 | 40.4 | 3.4 | 2059 | 9 | US-09-957-708-4 |

| | | | | | | |
|----|------|-----|------|----|---------------------|-------------------|
| 20 | 40.4 | 3.4 | 2394 | 10 | US-09-800-729-33 | Sequence 33, Appl |
| 21 | 40.2 | 3.4 | 2000 | 9 | US-09-938-842A-3966 | Sequence 3966, Ap |
| 22 | 40.2 | 3.4 | 3313 | 10 | US-09-764-846-83 | Sequence 83, Appl |
| 23 | 40.2 | 3.4 | 225 | 10 | US-09-925-299-744 | Sequence 744, App |
| 24 | 40.0 | 3.4 | 225 | 10 | US-09-925-299-744 | Sequence 744, App |
| 25 | 40.0 | 3.4 | 370 | 10 | US-09-960-352-5879 | Sequence 5879, Ap |
| 26 | 39.8 | 3.3 | 446 | 10 | US-09-960-352-3400 | Sequence 3400, Ap |
| 27 | 39.6 | 3.3 | 361 | 9 | US-10-125-258-108 | Sequence 108, App |
| 28 | 39.6 | 3.3 | 681 | 10 | US-09-822-830A-26 | Sequence 26, Appl |
| 29 | 39.6 | 3.3 | 166 | 10 | US-09-867-701-9636 | Sequence 9636, Ap |
| 30 | 39.4 | 3.3 | 302 | 9 | US-09-925-299-710 | Sequence 710, App |
| 31 | 39.4 | 3.3 | 1290 | 10 | US-09-925-299-710 | Sequence 710, App |
| 32 | 39.4 | 3.3 | 1290 | 10 | US-09-764-846-124 | Sequence 124, App |
| 33 | 39.2 | 3.3 | 227 | 10 | US-09-878-574-13011 | Sequence 13011, A |
| 34 | 39.2 | 3.3 | 229 | 10 | US-09-960-352-11338 | Sequence 11438, A |
| 35 | 39.2 | 3.3 | 3819 | 9 | US-09-978-295A-482 | Sequence 482, App |
| 36 | 39.2 | 3.3 | 3819 | 9 | US-09-978-295A-482 | Sequence 482, App |
| 37 | 39.2 | 3.3 | 3819 | 9 | US-09-978-697-482 | Sequence 482, App |
| 38 | 39.2 | 3.3 | 3819 | 9 | US-09-978-697-482 | Sequence 482, App |
| 39 | 39.2 | 3.3 | 3819 | 9 | US-09-978-697-482 | Sequence 482, App |
| 40 | 39.2 | 3.3 | 3819 | 9 | US-09-978-697-482 | Sequence 482, App |
| 41 | 39.2 | 3.3 | 3819 | 9 | US-10-028-072-405 | Sequence 405, App |
| 42 | 39.2 | 3.3 | 3819 | 9 | US-10-028-072-405 | Sequence 405, App |
| 43 | 39.2 | 3.3 | 3819 | 9 | US-10-123-904-405 | Sequence 405, App |
| 44 | 39.2 | 3.3 | 3819 | 9 | US-10-140-470-405 | Sequence 405, App |
| 45 | 39.2 | 3.3 | 3819 | 9 | US-10-175-746-405 | Sequence 405, App |
| | | | | | US-10-176-918-405 | Sequence 405, App |

ALIGNMENTS

RESULT 1
US-09-878-574-695
Sequence 695, Application us/09878574
Patent No. US20020110548A1
GENERAL INFORMATION:
APPLICANT: Byrium, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated w/
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 695
LENGTH: 252
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: LIB3028-047-Q1-B1-D12
US-09-878-574-695

Query Match 16.3%, Score 194.4; DB 10; Length 252;
Best Local Similarity 88.5%; Pred. No. 6e-40;
Matches 223; Conservative 0; Mismatches 26; Indels 3; Gaps 1;
192 AGAAGCTGACAGAGGATGCGAGGTTTTCGACGAGTCGTCGTTATGGAGACA 251
1 AAAATGCGACAGAGGATGCGAGGTTTTCGACGAGTCGTCGTTATGGAGACA 60
252 TTGGGGGACACATGACACATGCGTTTATGATCGATTCATCTTTGCGTTTGG 311
TTGGGGGACACATGACACATGCGTTTATGATCGATTCATCTTTGCGTTTGG 120
61 TTGGGGGACACATGACACATGCGTTTATGATCGATTCATCTTTGCGTTTGG 120
312 ATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 368
ATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
121 ATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
369 CTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 428
CTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
181 CTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240

CURRENT FILING DATE: 2001-09-24

```
; APPLICANT: Famodu, Omolayo O.  
; APPLICANT: Odell, Joan P.  
APPLICANT: _____  
APPLICANT: _____
```

RESULT 5
 US-10-078-929-65
 : Sequence 65. Application US/10078929
 : Patent No. US2002052497A1
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Rafalski, Antoni
 : APPLICANT: Miao, Guo-Hua
 : APPLICANT: Falco, Saverio Carl
 : APPLICANT: Sakai, Hajime
 : APPLICANT: Famodu, Omolayo O.
 : APPLICANT: Odell, Joan T.
 : APPLICANT: Meyers, Blake

```

RESULT 6
US-09-834-975-47/c
Sequence 47, Application US/09834975
Patent No. US20020110815A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Brown, Jeffrey
APPLICANT: Bolt, Andrew
APPLICANT: Van Huffel, Christophe
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
TITLE OF INVENTION: OF HUMAN CANCERS
FILE REFERENCE: MRL-016B
CURRENT APPLICATION NUMBER: US/09/834, 975
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/197,538
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 1046
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 47
LENGTH: 368
TYPE: DNA
ORGANISM: Homo sapiens

```

| | Query Match | Similarity | Best Local Matches | Conservative | Score 42.2; | Pred. No. 0.6; | Mismatches 143; | Indels 0; | Gaps 0 |
|----|-------------|--------------------------------------------------------------------|--------------------|--------------|-------------|----------------|-----------------|-----------|--------|
| QY | 918 | TGACATGAAGGGCTATCTTCACCTTGCAGTGACAAAAACGATAAAGACTT | 977 | | | | | | |
| Dd | 931 | TAAATATTAAAGGCGATCATTTTGCACAATGAGAAGTTAACTTCACTGTCTGAACGCTT | 990 | | | | | | |
| QY | 978 | TGCCATATGCCATTGATGANAAGAGGATACAAAAGATCTAATTAAGTTGCCATCATYA | 1037 | | | | | | |
| Dd | 991 | TGTATNATGAANAGTGATGAAGAGGGGTCTACTTCTTGAAGGGTTTTGCCCCACCAA | 1050 | | | | | | |
| QY | 1038 | CATGTGCAAACCTGATAATAANTGGAGAGCAGCATTTCTTTTAGCAATGACCAAGTTT | 1097 | | | | | | |
| Dd | 1051 | TCCTCATGATGAATGATGATTAATTGGTGAAGCCCCAAAAAAAAAAGCTTTTCGATGAAGAAAGAG | 1110 | | | | | | |
| QY | 1098 | CCAACAGTGCCTTATTTCGATAGTTGAGAACAAGAAAAATAATGAAGGGGGTG | 1157 | | | | | | |
| Dd | 1111 | AGAGGGTATCTTTTGTGGTCTTGCTCTATTAATGTGGATGAAGAAATGTGATTTGAACCTT | 1170 | | | | | | |
| QY | 1158 | TTTCGATTTTAAAAAIAAAAAAAAAAAAAAAAAA | 1188 | | | | | | |
| Dd | 1171 | ACTCGTAACTTAAAAAAAAAAAAAAAAAAAAA | 1201 | | | | | | |

```
RESULT 8
US-09-960-352-14060/c
; Sequence 14060, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(102981C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 14060
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 60-LIB3058-020-Q1-K1-G12
US-09-960-352-14060

Query Match          3.5%; Score 41.8; DB 10; Length 401;
Best Local Similarity 48.5%; Pred. No. 0.36;
Matches 115; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

OY 953 GGACAAAAACGATAAAGAGCGTTGCTATGCCATTGATAGAGAGATACAGAAA 1012
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 264 GAATAAAGGAATTTAAAGGGGTTTAAAGTCCCAAGGTGCAAGGTTGCAAAAA 205
OY 1013 GATTAATTAAGTTGCCATCATTAATGTCGAAAACCTGATAATGAGAGCAGCAT 1072
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 204 AAAAAAAGGTTTAAAGGAAAAAGAGGAAAGTTGAGATAGGTCGAGGGGTTT 145
OY 1073 TACTTTATGATGACCAAGCTTTCACAGCGTCGTTTATTTGATAGTGAAGAACAA 1132
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 144 AACCAAGTTTGACAAAAAATTTAAGACATTAAGCGAATTTTACCTGAAAAA 85
OY 1133 GAGAAAAAATATGAAGAGGGGTTTCGATTTTAAAAA 1189
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 84 AAAAAAAGGTTTAAAGGAAAAAGGAAAAA 28

RESULT 9
US-09-925-297-307
; Sequence 307, Application US/09925297
; Patent No. US20020081659A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA105
; CURRENT APPLICATION NUMBER: US/09/925,297
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05989
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; NUMBER OF SEQ ID NOS: 928
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 307
; LENGTH: 1046
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (14)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
```

```
; LOCATION: (946)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (946)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-297-307

Query Match          3.5%; Score 41.6; DB 10; Length 1046;
Best Local Similarity 51.7%; Pred. No. 0.63;
Matches 89; Conservative 1; Mismatches 82; Indels 0; Gaps 0;

OY 1018 AATTAAGTTGCCATCATTAATGTCGAAAACCTGATAATTAATGAGAGCAGATTACTT 1077
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 845 AAGTGAATGACCTTTTTCGATGAAATCTAAATCTTTGTAACCTTTTATATCTG 904
OY 1078 TTAATGAATGAACGAGTTTCCACAGGTCGTTTATTTGATGATGAGAAACAGACAA 1137
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 905 CTTTGTTCACCAAGAAACCTAAATCCTTTTAMNNANAAAAA 964
OY 1138 AATTAATGAAGGGGTTTCGATTTTAAAAA 1189
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 965 AAAAAAAGGTTTAAAGGAAAAAGGAAAAA 1016

RESULT 10
US-09-960-352-4582/c
; Sequence 4582, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION
; FILE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(102981C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 4582
; LENGTH: 393
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 20-LIB3057-013-Q1-K1-E7
US-09-960-352-4582

Query Match          3.5%; Score 41.4; DB 10; Length 393;
Best Local Similarity 48.5%; Pred. No. 0.46;
Matches 114; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

OY 955 ACAAAAAACGATAAAGAGCGTTGCTATGCCATGATGATAGAGGATACAGAAAAGA 1014
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 352 AAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 293
OY 1015 TCTAATTAAGTTGCCATCATTAATGTCGAAAACCTGATAATTAATGAGAGCAGATTTA 1074
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 292 TAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 233
OY 1075 CTTTATGAATGAACCAAGTTTCCACAGGTCGTTTATTTGATGATGAGAAACAGAA 1134
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 232 TATAATTAATTTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 173
OY 1135 GAAAAAATTAATGAAGGGGTTTCGATTTTAAAAA 1189
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 172 AAAAAAAGGTTTAAAGGAAAAAGGAAAAA 118

RESULT 11
US-09-925-297-303
; Sequence 303, Application US/09925297
; Patent No. US20020081659A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
```

```
QY      1104 GGTGCTTATTCATAGTGACAAACAAGAAAAATAAATGAAGGGCTTTGCAT 1163
          ||| | | | | | | | | | | | | | | | | | | | | |
Db      4754 GTTGTGTTTTCTTTTTTTTAATAACTCAAAAAAAAAATAAGAATTGGAGAA 4813
          ||| | | | | | | | | | | | | | | | | | | | | |
.QY     1164 TTTAAAAAAAAAAAAAAAAAAAAA 1189
          ||||| | | | | | | | | | | | | | | | |
```

| | | | | |
|---------------------------|--------|-----------------------------------------------------------|--------|-------------|
| Query Match | 3.48; | Score 41; | DB 10; | Length 419; |
| Best Local Similarity | 48.58; | Pred. No. 0.59; | | |
| Matches 113; Conservative | 0; | Mismatches 120; | Indels | 0; Gaps |
| QY | 957 | AAAAACGATRAAAGGAGCTTTGGCTATGCCATTGATGATAGGCGATCAAGAAAGATC | 1016 | |

```
DB 262 AAAAAAAAAATATATAAAAAAAAAATTTTATTTTATTTTATTTTATTTTATTTTACTT 203
OY 1017 TAATTAAGTTGCATCTACATGCGAAAACTGAATAAATGAGAGAGATTACT 1076
DB 202 TTTAAATTTTATTTATTTATTTTAAATAAAAAAAAAAAAAAAAAAAAAAAAAA 143
OY 1077 TTTATGAAATGACCAAGTTTCCACAGCTGTTTATTTTCGATAGTTGAAACAAAGAGA 1136
DB 142 AATTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 83
OY 1137 AAAAAATAATGAAGGCTGTTGATTTTAAATAAAAAAAAAAAAAAAAAA 1189
DB 82 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30
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RESULT 15

```
US-09-739-254-16
; Sequence 16, Application US/09739254
; Patent No. US20010021700A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 49 Human Secreted Proteins
; FILE REFERENCE: P2032P1
; CURRENT APPLICATION NUMBER: US/09/739,254
; EARLIER FILING DATE: 2000-12-19
; EARLIER APPLICATION NUMBER: 09/511,554
; EARLIER FILING DATE: 2000-02-23
; EARLIER APPLICATION NUMBER: PCT/US99/19330
; EARLIER FILING DATE: 1999-08-24
; EARLIER APPLICATION NUMBER: 60/097,917
; EARLIER FILING DATE: 1998-08-25
; EARLIER APPLICATION NUMBER: 60/098,634
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: Patentlin Ver. 2.0
; SEQ ID NO: 16
; LENGTH: 2608
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-739-254-16
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```
Query Match 3.4%; Score 41; DB 10; Length 2608;
Best Local Similarity 57.4%; Pred. No. 1.4;
Matches 74; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
```

```
OY 1061 GAGAGCAGGATTTATAGATGAACCAAGTTTCCACAGGTCGTTTATTTGATA 1120
DB 2441 GAGATGAGAGCTGATCTCGAAGCTGAAGACGCTTCAATTAACCAAGCTCTGGGAAA 2500
OY 1121 GTTGAGAACCAAGAAAAATATATGAAGGGGTTGTCATTTTAAATAAAAAAAAA 1180
DB 2501 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2560
OY 1181 AAAAAAAAA 1189
DB 2561 AAAAAAAAA 2569
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Search completed: March 18, 2003, 12:25:17
Job time : 121 secs
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GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 18, 2003, 17:36:17 ; Search time 38 Seconds
(without alignments)
1227.308 Million cell updates/sec

Title: US-09-857-613A-28

Perfect score: 1830
Sequence: 1 MATVRIPIITSCIHHTFPRS.....IEGYKKDLIKFAITTCRKE 350

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

Database:

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| 15: | /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:* |
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| 21: | /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:* |
| 22: | /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:* |
| 23: | /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:* |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|--------|-------------|--------|----|----------|---------------------|
| 1 | 1830 | 100.0 | 350 | 21 | AA196472 | Soybean gamma-toco |
| 2 | 1668.5 | 91.2 | 349 | 21 | AA196462 | Soybean gamma-toco |
| 3 | 1173 | 64.1 | 366 | 21 | AA196473 | Soybean gamma-toco |
| 4 | 1162 | 63.5 | 352 | 21 | AA196469 | Corn gamma-tocophe |
| 5 | 1154.5 | 63.1 | 348 | 21 | AA196469 | Arabidopsis thalia |
| 6 | 1154.5 | 63.1 | 348 | 23 | AA196462 | Herbicidally activ |
| 7 | 1151.5 | 62.9 | 308 | 21 | AA196462 | Arabidopsis thalia |
| 8 | 1151.5 | 62.9 | 348 | 20 | AA196462 | Arabidopsis thalia |
| 9 | 1151.5 | 62.9 | 348 | 21 | AA196462 | A. thaliana enviro |
| 10 | 1151.5 | 62.9 | 348 | 23 | AA196462 | A. thaliana gamma-t |

| | | | | | | |
|----|--------|------|-----|----|----------|--------------------|
| 11 | 1147.5 | 62.7 | 348 | 21 | AA196462 | Arabidopsis thali |
| 12 | 1144.5 | 62.5 | 308 | 21 | AA196462 | Arabidopsis thali |
| 13 | 1035.5 | 56.6 | 266 | 21 | AA196462 | Arabidopsis thali |
| 14 | 1028.5 | 56.2 | 266 | 21 | AA196462 | Arabidopsis thali |
| 15 | 1022.5 | 55.9 | 266 | 21 | AA196462 | Arabidopsis thali |
| 16 | 944 | 51.6 | 293 | 21 | AA196462 | Partial wheat gam |
| 17 | 778 | 42.5 | 191 | 21 | AA196462 | Corn gamma-tocoph |
| 18 | 673 | 36.8 | 172 | 21 | AA196462 | Rice gamma-tocoph |
| 19 | 647.5 | 35.4 | 317 | 20 | AA196462 | Synchocystis gam |
| 20 | 392 | 21.4 | 301 | 22 | AA196462 | Synchocystis PCC |
| 21 | 392 | 21.4 | 318 | 22 | AA196462 | Amino acid sequen |
| 22 | 392 | 21.4 | 318 | 22 | AA196462 | Synchocystis PCC |
| 23 | 392 | 21.4 | 318 | 22 | AA196462 | Synchocystis PCC |
| 24 | 392 | 21.4 | 318 | 23 | AA196462 | Synchocystis 2-m |
| 25 | 315 | 17.2 | 82 | 21 | AA196462 | Partial rice gam |
| 26 | 280.5 | 15.3 | 283 | 21 | AA196462 | S. lavendulae Mit |
| 27 | 265 | 14.5 | 81 | 22 | AA196462 | Physcomitrella pat |
| 28 | 257.5 | 14.1 | 128 | 21 | AA196462 | Rice gamma-tocoph |
| 29 | 254 | 13.9 | 280 | 18 | AA196462 | S-adenosyl methion |
| 30 | 232.5 | 12.7 | 285 | 21 | AA196462 | A. halophila sarc |
| 31 | 227 | 12.4 | 344 | 21 | AA196462 | Maize C-24 sterol |
| 32 | 226 | 12.3 | 279 | 21 | AA196462 | E. halochloris sal |
| 33 | 226 | 12.3 | 359 | 21 | AA196462 | Arabidopsis thali |
| 34 | 226 | 12.3 | 359 | 23 | AA196462 | Herbicidally acti |
| 35 | 224 | 12.2 | 144 | 21 | AA196462 | Partial rice gam |
| 36 | 222 | 12.1 | 115 | 21 | AA196462 | SAM dependent met |
| 37 | 220.5 | 12.0 | 275 | 20 | AA196462 | Spnf protein invo |
| 38 | 220.5 | 12.0 | 275 | 22 | AA196462 | S. spinosa protei |
| 39 | 217 | 11.9 | 344 | 20 | AA196462 | Corn SMT enzyme |
| 40 | 212.5 | 11.6 | 361 | 20 | AA196462 | Arabidopsis SMT e |
| 41 | 212.5 | 11.6 | 361 | 23 | AA196462 | Herbicidally acti |
| 42 | 207.5 | 11.3 | 346 | 23 | AA196462 | Nicotiana tabacum |
| 43 | 203.5 | 11.1 | 293 | 21 | AA196462 | Arabidopsis thali |
| 44 | 203.5 | 11.1 | 293 | 21 | AA196462 | Arabidopsis thali |
| 45 | 203.5 | 11.1 | 293 | 21 | AA196462 | Arabidopsis thali |

ALIGNMENTS

| | | |
|----------|---------------------------------------------------------------------|--------------------------------------------------------------------------|
| RESULT 1 | AA196472 | standard; Protein: 350 AA. |
| ID | AA196472 | |
| AC | AA196472 | |
| DT | 12-SEP-2000 | (first entry) |
| XX | | |
| XX | | Soybean gamma-tocopherol methyltransferase (clone sahlc.pK004.g2). |
| DE | | Vitamin E: alpha-tocopherol; biosynthesis; enzyme; inhibitor; herbicide; |
| XX | | gamma-tocopherol methyltransferase. |
| KW | | Glycine max. |
| OS | | |
| XX | | |
| PN | MO200032757-A2. | |
| PD | 08-JUN-2000. | |
| XX | | |
| PF | 02-DEC-1999; | 99WO-US28588. |
| XX | | |
| PR | 03-DEC-1998; | 98US-0110781. |
| XX | | |
| PA | (DUPO) DU PONT DE NEMOURS & CO E I. | |
| XX | | |
| PI | Cahoon RE, Coughlan SJ, Miao G, Rafalski JA; | |
| XX | | |
| DR | WPI: 2000-412309/35. | |
| DR | N-PSDB: AAA29164. | |
| XX | | |
| PT | Polynucleotide encoding a vitamin E biosynthetic enzyme polypeptide | |
| PT | such as gamma tocopherol methyltransferase, useful for synthesizing | |
| PT | vitamin E or as a target for design and discovery of herbicides | |

XX Claim 11; Page 65-66; 82pp; English.
 PS AAY96459-77 encode vitamin E (alpha-tocopherol) biosynthetic enzymes or
 CC their fragments. The cDNA clones were identified by BLAST searches based
 CC on similarity to Synecocystis sp. and Arabidopsis thaliana vitamin E
 CC biosynthetic enzymes. The enzymes are useful for synthesizing
 CC plastoquinones or tocopherols (especially vitamin E). Vitamin E is
 CC required for plant growth, therefore the enzymes may be used for the
 CC discovery of new herbicides. The enzymes can be used in methods to
 CC evaluate potential inhibitors, which may have use as herbicides.
 CC Additionally, transgenic expression of, e.g. gamma-tocopherol
 CC methyltransferase affords the ability to manipulate tocopherol levels as
 CC desired for a particular application.
 CC
 SQ Sequence 350 AA;
 Query Match 100.0%; Score 1830; DB 21; Length 350;
 Best Local Similarity 100.0%; Pred. No. 2e-172;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MATVRIPTISCIHHTFRSOSPRTFARIRVGRSMAPIRASASSEGEIVLEQPKKD 60
 DB 1 MATVRIPTISCIHHTFRSOSPRTFARIRVGRSMAPIRASASSEGEIVLEQPKKD 60
 QY 61 DKKIKQKIAEFTDESSGLMENIGDHHHGFYDSSTVSLSDHRAAQRMIQESLRPAS 120
 DB 61 DKKIKQKIAEFTDESSGLMENIGDHHHGFYDSSTVSLSDHRAAQRMIQESLRPAS 120
 QY 121 VSEERSKPKSTIVDVGCGIGSSRYLAKKPGATSVGITLSPVQORANALAAAGSLAKV 180
 DB 121 VSEERSKPKSTIVDVGCGIGSSRYLAKKPGATSVGITLSPVQORANALAAAGSLAKV 180
 QY 181 SFQVADALQOPFSDGQFDLVMSMESEHMPDKAKFVGEIARVAAGAIITIVTWCNRDLG 240
 DB 181 SFQVADALQOPFSDGQFDLVMSMESEHMPDKAKFVGEIARVAAGAIITIVTWCNRDLG 240
 QY 241 PDEOSLHPMEDDLKKICDAYLPAWCSTSDYVKLLQSLSDIDIKSEDMSRFVAFMPAV 300
 DB 241 PDEOSLHPMEDDLKKICDAYLPAWCSTSDYVKLLQSLSDIDIKSEDMSRFVAFMPAV 300
 QY 301 IRSATFWKGLSSLSGGKTIKALAMPIMTEGKKDLIKFAITTCRAPE 350
 DB 301 IRSATFWKGLSSLSGGKTIKALAMPIMTEGKKDLIKFAITTCRAPE 350
 RESULT 2
 AAY96462
 ID AAY96462 standard; Protein: 349 AA.
 AC AAY96462;
 XX 12-SEP-2000 (first entry)
 DE Soybean gamma tocopherol methyltransferase.
 XX
 KW Vitamin E: alpha-tocopherol; biosynthesis; enzyme; inhibitor; herbicide;
 KW gamma-tocopherol methyltransferase.
 OS Glycine max.
 XX WO200032757-A2.
 XX 08-JUN-2000.
 XX 02-DEC-1999; 99WO-US28588.
 XX 03-DEC-1998; 98US-0110781.
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 XX Cahoon RE, Coughlan SJ, Miao G, Rafalski JA;

DR WPI: 2000-412309/35.
 DR N-PSDB: AAA29154.
 XX Polynucleotide encoding a vitamin E biosynthetic enzyme polypeptide
 PT such as gamma tocopherol methyltransferase, useful for synthesizing
 PT vitamin E or as a target for design and discovery of herbicides
 XX
 PS Claim 11; Page 52-53; 82pp; English.
 XX
 CC AAY96459-77 show vitamin E (alpha-tocopherol) biosynthetic enzymes or
 CC their fragments. The cDNA clones were identified by BLAST searches based
 CC on similarity to Synecocystis sp. and Arabidopsis thaliana vitamin E
 CC biosynthetic enzymes. The enzymes are useful for synthesizing
 CC plastoquinones or tocopherols (especially vitamin E). Vitamin E is
 CC required for plant growth, therefore the enzymes may be used for the
 CC discovery of new herbicides. The enzymes can be used in methods to
 CC evaluate potential inhibitors, which may have use as herbicides.
 CC Additionally, transgenic expression of, e.g. gamma-tocopherol
 CC methyltransferase affords the ability to manipulate tocopherol levels as
 CC desired for a particular application.
 CC
 SQ Sequence 349 AA;
 Query Match 91.2%; Score 1668.5; DB 21; Length 349;
 Best Local Similarity 93.1%; Pred. No. 1.9e-156;
 Matches 323; Conservative 5; Mismatches 10; Indels 9; Gaps 1;
 QY 1 MATVRIPTISCIHHTFRSOSPRTFARIRVGRSMAPIRASASSEGEIVLEQPKKD 60
 DB 1 MATVRIPTISCIHHTFRSOSPRTFARIRVGRSMAPIRASASSEGEIVLEQPKKD 60
 QY 61 DKKIKQKIAEFTDESSGLMENIGDHHHGFYDSSTVSLSDHRAAQRMIQESLRPAS 120
 DB 61 DKKIKQKIAEFTDESSGLMENIGDHHHGFYDSSTVSLSDHRAAQRMIQESLRPAS 120
 QY 121 VSEERSKPKSTIVDVGCGIGSSRYLAKKPGATSVGITLSPVQORANALAAAGSLAKV 180
 DB 121 VSEERSKPKSTIVDVGCGIGSSRYLAKKPGATSVGITLSPVQORANALAAAGSLAKV 180
 QY 241 PDEOSLHPMEDDLKKICDAYLPAWCSTSDYVKLLQSLSDIDIKSEDMSRFVAFMPAV 300
 DB 241 PDEOSLHPMEDDLKKICDAYLPAWCSTSDYVKLLQSLSDIDIKSEDMSRFVAFMPAV 300
 QY 301 IRSATFWKGLSSLSGGKTIKALAMPIMTEGKKDLIKFAITTCRAPE 347
 DB 301 IRSATFWKGLSSLSGGKTIKALAMPIMTEGKKDLIKFAITTCRAPE 338
 RESULT 3
 AAY96473
 ID AAY96473 standard; Protein: 366 AA.
 AC AAY96473;
 XX 12-SEP-2000 (first entry)
 DE Soybean gamma-tocopherol methyltransferase.
 XX
 KW Vitamin E: alpha-tocopherol; biosynthesis; enzyme; inhibitor; herbicide;
 KW gamma-tocopherol methyltransferase.
 OS Triticum aestivum.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 5 /note= "encoded by GNC"
 FT Misc-difference 45 /note= "encoded by CNG"
 XX

PN MO200032757-A2.
XX
PD 08-JUN-2000.
XX
PE 02-DEC-1999; 99MO-US28568.
XX
PR 03-DEC-1998; 98US-0110781.
XX
PA (DDPO) DU PONT DE NEMOURS & CO E.I.
XX
P1 Cahoon RE, Coughlan SJ, Miao G, Rafalski JA;
P1 MPI: 2000-412309/35.
DR
DR N-PSDB; AAA29165.
XX
XX Polynucleotide encoding a vitamin E biosynthetic enzyme polypeptide
PT such as gamma tocopherol methyltransferase, useful for synthesizing
PT vitamin E or as a target for design and discovery of herbicides
XX
XX
PS Clalm 11; Page 67-68; 82pp; English.

XX
XX AAY96459-77 encode vitamin E (alpha-tocopherol) biosynthetic enzymes or
CC their fragments. The cDNA clones were identified by BLAST searches based
CC on similarity to Synecocystis sp. and Arabidopsis thaliana vitamin E
CC biosynthetic enzymes. The enzymes are useful for synthesizing
CC plastoquinones or tocopherols (especially vitamin E). Vitamin E is
CC required for plant growth, therefore the enzymes may be used for the
CC discovery of new herbicides. The enzymes can be used in methods to
CC evaluate potential inhibitors, which may have use as herbicides.
CC Additionally, transgenic expression of, e.g. gamma-tocopherol
CC methyltransferase affords the ability to manipulate tocopherol levels as
CC desired for a particular application.
XX
SQ Sequence 366 AA;

RESULT 5
AAG51381
ID AAG51381 standard; Protein: 348 AA.
XX AAG51381;
AC AAG51381;
XX
DT 18-OCT-2000 (first entry)
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65206.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hydridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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PR 25-FEB-1999; 99US-0121825.
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 Best Local Similarity 69.4%; Pred. No. 1.4e-105;
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DB 81 DHMHGFGTSDSTVSLSD--HRAAQIRMTQESLRFPASVS--EERSKMPKSIYVGGGIGGS 140
QY 143 SHYLAKKFGATSVGIGTLSPVQARANALAAAGLADKVSFOVADALQOPFSDGQFDLVMS 202
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QY 203 MESGEHMPDKAKFVCEGLARVAPGAILIIVTCHRDLPDQSLHPWEDLLKRICDARY 262
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QY 263 LPANCSTSDYKLLQSLSDQIKSEDSRFPAPFPVIRAFVTKGSLSSGOKTIK 322
DB 261 LPANCSTDDYVNLQSHSLQDKADWSENVAPFPVIRAFVTKGSLSSGOKTIK 320
QY 323 GALAMPMEIGYKKDLIKFAITTCRKP 349
DB 321 GALTPLMEIGYKKGVIRFGIITCOCKP 347

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RESULT 6

ABB91452 standard; protein; 348 AA.

ABB91452;

31-MAY-2002 (first entry)

Herbicide; active polypeptide SEQ ID NO 663.

Herbicide; plant; agriculture; herbicide.

Arabidopsis thaliana.

WO200210210-A2.

07-FEB-2002.

28-AUG-2001; 2001WO-EP09892.

28-AUG-2001; 2001WO-EP09892.

(FARB) BAYER AG.

Tietjen K, Weidner M;

WPI; 2002-269010/31.

Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms -

Claim 5; SEQ ID NO 663; 261pp + Sequence Listing; English.

The invention relates to identifying target proteins

(ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as herbicides.

Sequence 348 AA;

Query Match 63.1%; Score 1154.5; DB 23; Length 348;
 Best Local Similarity 69.4%; Pred. No. 1.4e-105;
 Matches 227; Conservative 28; Mismatches 61; Indels 11; Gaps 4

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QY 32 GPRNAPIRASASSE-----RGEIVLEOKRKDDKKLQKGLAEFYDESSGLWENING 85
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QY 86 DHMHGFGTSDSTVSLSD--HRAAQIRMTQESLRFPASVS--EERSKMPKSIYVGGGIGGS 142
DB 81 DHMHGFGTSDSTVSLSD--HRAAQIRMTQESLRFPASVS--EERSKMPKSIYVGGGIGGS 140
QY 143 SHYLAKKFGATSVGIGTLSPVQARANALAAAGLADKVSFOVADALQOPFSDGQFDLVMS 202
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| Db | 10 | VAAATSTSE-----AARKGIAEFYNETSGIMEIINGDHMHGIFYDPS | 53 | |
| Oy | 99 | VSLSD--HRAAQIRMIOESLRPASVS--EERSKMPKSIYDVGCGIGSSRYLAKKGQANSV | 155 | |
| Db | 54 | VOLSDSGHKEAQIRMIEESIRFAGVTDEEKEKKIKRYVDVGCIGGSSRYLAKGAECI | 113 | |
| Oy | 156 | GTTTSPVOQANMLAAAGLADKVSQVADALDQPEFSOQPELVMSMSGEMPPKAF | 215 | |
| Db | 114 | GTTTSPVOAKRANDLAAQSLAHKASFQVADALDQPEDEKPELVMSMSGEMPPKAF | 173 | |
| Oy | 216 | VGELARVAPACAIITITWCHRDGPPEOSLHWEODLKKICIDAVYLRPMCSSTDYVNL | 275 | |
| Db | 174 | VKELVRVAAPEGRITITWCHRNLSAGEALQPMQNIIDKICKTFEYLRPMCSSTDYVNL | 233 | |
| Oy | 276 | LOSLSLQDIKSEDSRFVAPPVAVIRSAFTWTKGLSSLSGQKTIKCALMPMIETGK | 335 | |
| Db | 234 | LOSHSLQDIKCADSENVAVFPVIRTALTWTKGLVSLRSQKSIKCALTPMLMIEGK | 293 | |
| Oy | 336 | KDLIKFATITCRKP 349 | | |
| Db | 294 | KGVIKFGITTCOKP 307 | | |
| RESULT 8 | | | | |
| AAW95017 | ID | AAW95017 standard; Protein: 348 AA. | | |
| XX | AAW95017; | | | |
| AC | 21-MAY-1999 | (first entry) | | |
| XX | | | | |
| DE | Arabidopsis gamma-tocopherol methyltransferase (gamma-TMT). | | | |
| XX | | | | |
| KW | Gamma-tocopherol methyltransferase; gamma-TMT; SLR0089; 165H577; meat | | | |
| KM | transgenic plant; alpha-tocopherol; gamma-tocopherol; forage plant. | | | |
| XX | | | | |
| OS | Arabidopsis sp. | | | |
| XX | | | | |
| PM | W09904622-A1. | | | |
| XX | | | | |
| PD | 04-FEB-1999. | | | |
| XX | | | | |
| PF | 22-JUL-1998; 98WO-US15137. | | | |
| XX | | | | |
| PR | 17-JUL-1998; 98US-0053819. | | | |
| PR | 25-JUL-1997; 97US-0053819. | | | |
| PR | 26-JAN-1998; 98US-0072497. | | | |
| XX | | | | |
| PA | (UYNE-) UNIV NEVADA. | | | |
| XX | | | | |
| PI | Dellapenna D, Shintani DK; | | | |
| XX | | | | |
| DR | WPI; 1999-142456/12. | | | |
| DR | N-PSDB; AAX17789. | | | |
| XX | | | | |
| PT | Newly isolated DNA fragment comprising a ^c-tocopherol (vitamin E) | | | |
| PT | methyltransferase coding sequence - useful for producing | | | |
| PT | ^a-tocopherol, and transgenic plants, seeds and oils with an altered | | | |
| XX | tocopherol profile | | | |
| PS | | | | |
| XX | Example 5; Page 36-38; 46pp; English. | | | |
| CC | The invention provides DNA sequences encoding gamma-tocopherol | | | |
| CC | methyltransferases (gamma-TMT). The gamma-TMT encoding genes SLR0089 | | | |
| CC | and 165H577 are isolated from <i>Synechocystis</i> and <i>Arabidopsis</i> species | | | |
| CC | respectively. The DNA fragments are useful for producing transgenic | | | |

PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
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PR 21-JUL-1999; 99US-0145086.
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PR 22-JUL-1999; 99US-0145085.
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PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145102.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
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PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
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PR 07-SEP-1999; 99US-0152363.
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PR 13-SEP-1999; 99US-0153758.
PR 13-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
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PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 13-OCT-1999; 99US-0159329.
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PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
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PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 62.7%; Score 1147.5; DB 21; Length 348;
Best Local Similarity 68.8%; Pred. No. 6.9e-105;
Matches 225; Conservative 30; Mismatches 61; Indels 11; Gaps 4;

QY 32 GPRSWAPIRASASSE-----RGEIVLEQKRKKDDKKLQKGLAEFYDESSGLWENING 85
DB 23 GSKSSILFRPSSSSSVSMWTTRGNVAVAAATSTE--ALRRGIAEFYNETSGLWEEIING 80

QY 86 DHMHGFYDSDSTVSLSD--HRAAOIRMOESLRFASVS--EERSWKPKSIYVGGIGGS 142
DB 81 DHMHGFYDSDSVOLSDSGHKEAOIRMEESLRFAGVDEDEEKIKIKVNVVGGIGGS 140

QY 143 SKYLAKKFGATSVGTTLSFPVQORANALAAAGLADKVSFOYADALQOPFSGOPFLVMS 202
DB 141 SKYLAKKFGAEGICITLTSVPQAKRANDLAAQSLSHKASFOYADALDKRFEDGKFDLVMS 200

QY 203 MESGEMPDKAKFVGEELARVAAPGAIITIIYVTCNRDLGFDSESLHPMEDLLKKTIDAY 262
DB 201 MESGEMPDKAKFVKELELVAAVAGRIIIVTCNRLSGEALQPMWEGNIIDKICKTFFY 260

QY 263 LPACSTSDYVKLLQSLSLQDIKSEDMSEFVAPFVPAVIRSAFTYWKGLSSLSGOKTK 322
DB 261 LPACSTDDYVLLQSLSLQDIKCADMSENVAPFVPAVIRTALTYWKGLVSLRSKMSIK 320

QY 323 GALAPLMIEGKKDLIRFAIITCRKP 349
DB 321 GALTWPLMIEGKKGVIRKGIITCOKP 347

RESULT 12
AAG07857
ID AAG07857 standard; Protein: 308 AA.
XX
XX AAG07857;
XX
XX 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 5169.
XX
XX Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
XX Arabidopsis thaliana.
OS
XX
XX EPI033405-A2.
PN
XX
XX 06-SEP-2000.
PD
XX
XX
XX 25-FEB-2000; 2000EP-0301439.
PF
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125768.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
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PR 19-APR-1999; 99US-0130077.
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PR 23-APR-1999; 99US-0130891.
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PR 01-JUL-1999; 99US-0141842.
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PR 06-JUL-1999; 99US-0142055.
PR 08-JUL-1999; 99US-0142390.
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PR 22-JUL-1999; 99US-0145085.
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PR 27-JUL-1999; 99US-0145918.
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PR 02-AUG-1999; 99US-0146389.
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PR 06-AUG-1999; 99US-0147416.
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PR 10-AUG-1999; 99US-0148171.
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PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
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PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.

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PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
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PR 07-OCT-1999; 99US-0158029.
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PR 12-OCT-1999; 99US-0158369.
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PR 21-OCT-1999; 99US-0160741.
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PR 28-OCT-1999; 99US-0161920.
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PR 29-OCT-1999; 99US-0162142.
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Query Match 62.5%; Score 1144.5; DB 21; Length 308;
Best Local Similarity 70.7%; Pred. No. 1,2e-104; Indels 19; Gaps 3;
Matches 222; Conservative 26; Mismatches 47;

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DB 10 VAAATSTE-----ALRKGIAEFYNETSGLWEETJGDMHGHGFDPDSS 53
OY 99 VLSLD--HRAOIRMIQESLRASVS--FEERSKWPMSIYDVCGGIGSSRYLAKKFGAIVS 155
DB 54 VOLSNGHKEAOIRMIESTLRAGVTDDEEEKKIRKVVYDVGCGIGSSSYLASKGAGACI 113
OY 156 GTTSPVOAKRANALAAAGLADKVSFOVADALLOPFSDGQFDLYWSMESGEHMPDKAKF 215
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DB 114 GTTSPVOAKRANALAAASLSHKASFOVADALDKPFEDGKFDLYWSMESGEHMPDKAKF 173
OY 216 VGLARVAAPAGAIITIVWCHRDLPDEQSLHPWEDDLKIKIDAVYILPAMCSTSDYVL 275
DB 174 VVELRVAAAPGRIITIVWCHRNLSAGEEALQPMEDNIIIDKICTFYLLPAMCSTDYVNL 233
OY 276 LOSLSLDIKSEDMGRFPAFPWPAYIRSAFTWKGLSSLLSGCKITKALAMPIMIEGK 335
DB 234 LOSLSLDIKCADWSEENAFWPAYIRFALTWKGLVSLRSKMSIKGALTPLMIEGK 293
OY 336 KDLIKFAIITCKRP 349
DB 294 KGVIKFGIITCKP 307

RESULT 13
AAG51383
ID AAG51383 standard; Protein: 266 AA.
XX AAG51383;
AC
XX
DF 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65208.
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
OS Arabidopsis thaliana.
XX EP1033405-A2.
PN
XX
PD 06-SEP-2000.
XX
PE 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
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PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 16-APR-1999; 99US-0128714.
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PR 23-APR-1999; 99US-0130510.
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PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
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PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
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PR 08-JUN-1999; 99US-0138094.
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PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
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PR 18-JUN-1999; 99US-0139456.
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PR 18-JUN-1999; 99US-0139458.
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PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 30-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
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PR 29-OCT-1999; 99US-0162142.

Query Match

56.6%; Score 1035.5; DB 21; Length 266;

Best Local Similarity 75.8%; Pred. No. 5,7e-94; Matches 201; Conservative 18; Mismatches 43; Indels 3; Gaps 2;

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AC AAG07858;
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DT 17-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
XX
XX Arabidopsis thaliana.
OS
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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DB 121 SEHMPDKRKFVGEELARVAPAGATIIIVTWCHRNLSAGEALQPEQNTLDKICTFYLP 180
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DB 181 AMCSYDDYVNLQSLSDIDKADMSENVAFPMFPAVIRALWKGVLVSLRSGMSKICA 240
QY 325 LAMPIMIEGKKDLIKFAITTCRK 349
DB 241 LAMPIMIEGKKVIFKGIITCOKP 265

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DT 21-SEP-2001 (first entry)
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DE Physcomitrella patens 78_pppocl.087_e12-259rev protein.
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KW Tocopherol and carotenoid metabolism related protein; TCMP; synthesis;
KW Physcomitrella patens; moss; algae; microorganism; fungus; plant;
KW identification; genome mapping; modulation; evolutionary study;
KW cellular production; fine chemical.
XX
OS Physcomitrella patens.
XX
PN WO200144276-A2.
XX
PD 21-JUN-2001.
XX
PF 14-DEC-2000; 2000WO-EP12698.
XX
PR 16-DEC-1999; 99US-0171121.
XX
PA (BADI ) BASF PLANT SCI GMBH.
XX
PI Lerchl J, Renz A, Ehrhardt T, Reindl A, Clippus P, Bischoff F,
PI Frank M, Freund A, Duvenig E, Schmidt R, Reski R, Badur R;
XX
DR WPI: 2001-398121/42.
DR N-PSDB: AAH44261.
XX
XX Tocopherol and carotenoid metabolism related protein (TCMP), used to
XX produce fine chemicals, is isolated from mosses, algae, microorganisms,
XX fungi, plants, or their fragments -
XX Claim 28; Page 122; 123pp; English.
XX
CC The present invention describes isolated tocopherol and carotenoid

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CC metabolism related proteins (TCMRP) (I) from mosses or algae.
CC microorganisms or fungi, plants, or its fragments. (I) can be used as
CC enzymes in the production of fine chemicals or in the metabolism of
CC tocopherols and carotenoids. (I) also assist in transmembrane transport.
CC The fine chemicals that can be produced include lipids, fatty acids,
CC vitamins, cofactors, enzymes, amino acids, and nucleotide bases.
CC Nucleotide sequences, proteins, vectors and host cells from the present
CC invention can be used: (a) to identify mosses related to Physcomitrella
CC patens; (b) in mapping genomes of mosses related to Physcomitrella
CC patens; (c) in the modulation of TCMRP activity; (d) in evolutionary
CC studies; (e) in the determination of functional TCMRP regions; (f) and
CC in the cellular production of fine chemicals. AAH44222 to AAH44262
CC encode the Physcomitrella patens TCMRP proteins given in AAB99849 to
CC AAB99889. AAH44212 to AAH44221 represent nucleotide sequence used in
CC the exemplification of the present invention.
XX
S0 Sequence 370 AA;

Query Match 55.9%; Score 1022.5; DB 22; Length 370;
Best Local Similarity 59.4%; Pred. No. 1.8e-92;
Matches 208; Conservative 40; Mismatches 81; Indels 21; Gaps 6;

QY 11 SCIHHTFRSOSPRTFARI-----RVCPRSMAPIRASASRGEIVLEQPKKDDK 62
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QY 63 KKLQGIAEFYDESSGLWENIWDHMHGFDSDSTVSL---SDHRAQIRMIQESLRF 118
DB 79 PELYDGIAEFYDESSGVEGIEGHEMHGYDEIVEAVDDPDHRRQIMIKESLAY 138

QY 119 ASVSEERSKMPKSIYDVGCGIGSSRYLAKKFGATSVGTTSPVOAQRANALAAQGLAD 178
DB 139 AGVPDSKDLKPTIYDVGCGIGSSRYLAKKFGATSVGTTSPVOAQRANALAAQGLAD 198

QY 179 KVSFOVADALQPFSDGQFDLVMSMESGHEMDKAFVGEARVAAPGAIITITVWCHRD 238
DB 199 LNVFOVANAALNPFODGSDLDLVMSMESGHEMDKAFVGEARVAAPGAIITITVWCHRD 258

QY 239 LGPDEOSLHPWEDDLKIKICDAYVLPAMCSTSDYVKLQSLSLQDIKSEDMGRFVAPFP 298
DB 259 LKPGETSLKPDQDLKICDAFYLPAMCSPSDYVSIKDKLQDIKSEDMGRFVAPFP 318

QY 299 AVIRSAFTWKGISLLSGQKTIKAGALAMPIMEGYKKDLIKFAIITCRK 348
DB 319 AVMTKALSMEGIVLKGSGMTWKGAFAMTLMIGYGRGLIKFAAITCRK 368

Search completed: March 18, 2003, 17:37:06
Job time : 40 secs

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Db      201 PKLEGVSEIYKLRKGFAPVAYEWMTDKYDENNEH-----RKI--AVEIELGDGI 251
Oy      264 PWCSTSDYVKLLQSLSDIKSED-----NSRFAPFMPVAY-----IRSAF 305
Db      252 PMFHVDAVKAKLKNCGFEVLVSEDLADNDEIPWYPTLGEKRYQVQNLANLATEFFRTSY 311
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RESULT 8 US-09-041-718-2

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; Sequence 2, Application US/09041718A
; Patent No. 6225075
; GENERAL INFORMATION:
; APPLICANT: Bard, Martin
; TITLE OF INVENTION: DNA encoding sterol methyltransferase
; FILE REFERENCE: 740.003US1
; CURRENT APPLICATION NUMBER: US/09/041,718A
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-041-718-2

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Query Match      10.3%; Score 189; DB 4; Length 376;
Best Local Similarity 21.6%; Pred. No. 5,7e-12;
Matches 74; Conservative 55; Mismatches 133; Indels 80; Gaps 13;

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Oy      59 KDDKKIKLGIAE-----FDSESSGLMENWGMHMG-FYDSDS--TVSLSDHRAAQIR 110
Db      59 KODEKRLNDYSQLTGHYHYNLWTDFFEYGVGSSFFHSRYKCEAFQATARHGHFAHQM 118
Oy      111 MIOESLRFASVSEERSKWPFSIVDVCIGSSSRYLAKKFGATSVGITLSPVOAORANL 170
Db      119 NINENMK-----VLVDGCGVGGPGRRETRTDEIYGLNNNDYQIERANHY 164
Oy      171 AAAGLADKVSFOVADALQPFSDGFDLWMSGESGEMPDRAKFGVGLARVAAPGAIIT 230
Db      165 AKKYHLDKRLSYKGDPMDFEPESFDVAVAIEATVHAPVLEGVYSELYVKLPGGIRG 224
Oy      231 IYTWK-----HRLG-----PDEQSLH--PWEDOLKIKICA- 260
Db      225 VEWMTDKYDETNEHRIAYGIEVGDIIPKYSRKVAEOALKNVGFIEYOKDLADVD 284
Oy      261 ----YILP-----AMCST-SDYVKLLQSLSDIKSEDSMRVAPFMPVAYSAFTWKGL 310
Db      285 DEIPWYPTLSDGLKFCQRTGDIYVPRISRI-----GRITTESVGLMEKI----- 330
Oy      311 SSLSSGQTKIGAL---AMPLMIEGYKKDLIKFAITTCRKP 349
Db      331 GLAPKSGKQVTHALEDAVNLVEGGKQLFTPMPLVYVARKP 371

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RESULT 9 US-09-036-987A-13

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; Sequence 13, Application US/09036987A
; Patent No. 6143526
; GENERAL INFORMATION:
; APPLICANT: Baltz, Richard H.
; APPLICANT: Broughton, Mary C.
; APPLICANT: Crawford, Kathryn P.
; APPLICANT: Madduri, Krishnamurthy
; APPLICANT: Merlo, Donald J.
; APPLICANT: Treadway, Patli J.

```

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; APPLICANT: Turner, Jan R.
; APPLICANT: Waldron, Clive
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
; TITLE OF INVENTION: Production
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dow Agrosciences LLC Patent Department
; STREET: 9350 Zionsville Road
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/036,987A
; FILING DATE: 09-MAR-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stuart, Donald R.
; REGISTRATION NUMBER: 28,479
; REFERENCE/DOCKET NUMBER: 50,608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317)337-4816
; TELEFAX: (317)337-4847
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 283 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-036-987A-13

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Query Match      8.3%; Score 152.5; DB 4; Length 283;
Best Local Similarity 24.2%; Pred. No. 3.3e-08;
Matches 48; Conservative 28; Mismatches 77; Indels 45; Gaps 4;

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Oy      85 GDHMHGFYD-----SDSTVSLSDHRAAQIRMIQESLRFASVSEERSKWPFSI 132
Db      11 GPRLHGWYAGGYREDACATPMSDADQLTD-----LFLDKALIRGA-----HL 55
Oy      133 YDVGGIGGSSRYLAKKFGATSVGITLSPVOAORANALAAAGLADKVSFOVADALQPF 192
Db      56 FDLGGGNOQPVYRACASGVRTGITVNAQHILAAATRLANETGLAGSLFELVDGAQLPY 115
Oy      193 SDGQFDLWMSGESGEMPDRAKFGVGLARVAAPGAIITITVWCHRDIGPDEOSLHPWED 252
Db      116 PDGFOAMAMQSVQVQIDQAAAIREVHRILEPGRFVLDIITRVRLPEE----- 166
Oy      253 LTKKICDAVYLPWCSTS 270
Db      167 -----YAAVWTGTT 175

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RESULT 10 US-09-370-700-13

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; Sequence 13, Application US/09370700
; Patent No. 6274350
; GENERAL INFORMATION:
; APPLICANT: Baltz, Richard H.
; APPLICANT: Broughton, Mary C.
; APPLICANT: Crawford, Kathryn P.
; APPLICANT: Madduri, Krishnamurthy
; APPLICANT: Treadway, Patli J.
; APPLICANT: Turner, Jan R.
; APPLICANT: Waldron, Clive
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
; FILE REFERENCE: 50489 DIV1
; CURRENT APPLICATION NUMBER: US/09/370,700
; CURRENT FILING DATE: 1999-08-09

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: ORGANISM: Escherichia coli
US-08-457-245-9

Query Match      8.3%; Score 152; DB 1: Length 282;
Best Local Similarity 24.1%; Pred. No. 3.7e-08;
Matches 61; Conservative 40; Mismatches 94; Indels 58; Gaps 12;

OY 71 EFVDESSGLWMININGDDHHNG---FYDSDTVYSLSDHRAAOLRMIOESLRFASVSEERSK 127
   1 1 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 18 EHYDLGNLFERMLDPFQOYSCATWKDD---NLESAGQAKLMKICEKLQ-----K 66
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

OY 128 WPKSLVDVCGGSGSSRYLAKKFGATSVGITLSPVOAQRANALAAAGLADKVSFOVADA 187
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 67 PGMRLVDIGCGMGGLAHYMASNYDVSVGVITISAEQKMAQ--ERCEGLDVTI----- 117
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

OY 188 LQQPESD--GQFDLWMSHESGEHMPDK--AKFVGLARVAAPGAIITVTWCHROLGDPDE 243
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 118 LLDYRDLNDQDFDRIVSVGMFEHGRPKNYDYFFAVVDNRKLREGIFLLHT-----IGSKK 172
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

OY 244 QSLH--PWEQDLKTKICQAYYLPANCSTSDYVKLLQSLDQIKSEDSRFAVP----- 296
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 173 TDLNADPW-----INKITFPNGCLPS--VKIOASSEPFVEMDHNFAGADYDTILM 222
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

OY 297 -----MPAV 300
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 223 AMYERFLAAMPEI 235
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

RESULT 12
US-09-355-166-20
; Sequence 20 Application US/09355166
; Patent No. 6316241
; GENERAL INFORMATION:
; APPLICANT: Genencor International, Inc.
; TITLE OF INVENTION: Alpha/Beta Hydrolase-Fold Enzymes
; FILE REFERENCE: GC511-PCF
; CURRENT APPLICATION NUMBER: US/09/355,166
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Bacillus
US-09-355-166-20

Query Match      5.9%; Score 107.5; DB 4: Length 233;
Best Local Similarity 28.1%; Pred. No. 0.0018;
Matches 45; Conservative 24; Mismatches 74; Indels 17; Gaps 6

OY 132 IYDVCGGIGSSRYLAKKFGATSVGITLSPVOAQRANALAAAGLADKVSFOVADALQOP 191
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 39 ILDAGGCGTGAAYLGHLLPYTV-VDRKPIMLEKAKRFPANEGLA--IPAYQAELEHLP 95
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

OY 192 FSDGQFDLWMSHESGEHMPDKAKFVGLARVAAP-GAIITVTWCHROLGDPDEQSLHPE 250
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 96 FSESSESCVLS-ESVLSFSRLTSSLOEISRYLKPSCMLGIEAALKKPMPPAEK----- 148
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

OY 251 QDLKTKICQAYYLPANCSTSDYVKLLQSLDQIKSEDS 290
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 149 ----KOMDPFGFTCLHESSEHMKLRSYGFO--KTEAMS 182
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

RESULT 13
US-08-576-626A-56
; Sequence 56 Application US/08576626A
; Patent No. 5998194
; GENERAL INFORMATION:
; APPLICANT: Summers, R.G.
; APPLICANT: Katz, L.
; APPLICANT: Donadio, S.
; APPLICANT: Staver, M.J.
; TITLE OF INVENTION: POLYKETIDE-ASSOCIATED SUGAR

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GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: March 18, 2003, 17:38:15 ; Search time 15 Seconds

(without alignments)
1075.482 Million cell updates/sec

Title: US-09-857-613A-28

Perfect score: 1830
Sequence: 1 MATVVRIPITISCHIRIFRS.....IEGKKDLIRFAITCKRPE 350

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 199416 seqs, 46092074 residues

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PC1_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/PCYUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|------------------------|---------------------|
| 1 | 225 | 12.3 | 344 | 10 US-09-779-144A-7 | Sequence 7, Appli |
| 2 | 212.5 | 11.6 | 361 | 10 US-09-779-144A-4 | Sequence 4, Appli |
| 3 | 203.5 | 11.1 | 383 | 10 US-09-801-368-96 | Sequence 96, Appli |
| 4 | 203.5 | 11.1 | 383 | 10 US-09-779-144A-2 | Sequence 2, Appli |
| 5 | 141 | 7.7 | 251 | 9 US-10-260-877-54 | Sequence 54, Appli |
| 6 | 139 | 7.6 | 451 | 9 US-09-738-626-4136 | Sequence 12084, A |
| 7 | 139 | 7.6 | 451 | 10 US-09-845-248-2 | Sequence 2, Appli |
| 8 | 117.5 | 6.4 | 206 | 9 US-09-738-626-4923 | Sequence 4923, Ap |
| 9 | 112 | 6.1 | 251 | 9 US-09-738-626-6365 | Sequence 6365, Ap |
| 10 | 110 | 6.0 | 218 | 9 US-09-738-626-4999 | Sequence 4999, Ap |
| 11 | 107.5 | 5.9 | 233 | 10 US-09-950-368-10 | Sequence 20, Appli |
| 12 | 105 | 5.7 | 256 | 10 US-09-815-242-12004 | Sequence 12084, A |
| 13 | 105 | 5.7 | 348 | 10 US-09-939-521-11 | Sequence 11, Appli |
| 14 | 99 | 5.4 | 241 | 10 US-09-815-242-12602 | Sequence 12602, A |
| 15 | 98.5 | 5.4 | 234 | 10 US-09-815-242-5314 | Sequence 5314, Ap |
| 16 | 97 | 5.3 | 266 | 12 US-10-007-693-66 | Sequence 66, Appli |
| 17 | 95.5 | 5.2 | 255 | 9 US-09-866-050A-706 | Sequence 706, Appli |
| 18 | 94.5 | 5.2 | 273 | 10 US-09-816-714-4 | Sequence 4, Appli |
| 19 | 94.5 | 5.2 | 680 | 9 US-09-738-626-4877 | Sequence 4877, Ap |

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|----|------|-----|------|------------------------|--------------------|
| 20 | 92 | 5.0 | 7968 | 9 US-10-077-130-5 | Sequence 5, Appli |
| 21 | 91.5 | 5.0 | 2201 | 9 US-10-085-476-2 | Sequence 2, Appli |
| 22 | 91.5 | 5.0 | 2201 | 12 US-10-029-907-3 | Sequence 3, Appli |
| 23 | 90.5 | 4.9 | 828 | 10 US-09-816-685-4 | Sequence 4, Appli |
| 24 | 90 | 4.9 | 1832 | 9 US-10-014-717-4 | Sequence 4, Appli |
| 25 | 89.5 | 4.9 | 257 | 9 US-09-738-626-6656 | Sequence 6656, Ap |
| 26 | 89 | 4.9 | 2894 | 10 US-09-941-611-23 | Sequence 23, Appli |
| 27 | 89 | 4.9 | 3011 | 10 US-09-916-359-2 | Sequence 7, Appli |
| 28 | 88.5 | 4.8 | 448 | 10 US-09-939-521-7 | Sequence 7, Appli |
| 29 | 88 | 4.8 | 207 | 10 US-09-921-397-94 | Sequence 94, Appli |
| 30 | 88 | 4.8 | 3011 | 9 US-09-747-419-20 | Sequence 20, Appli |
| 31 | 88 | 4.8 | 3011 | 9 US-09-891-894-3 | Sequence 3, Appli |
| 32 | 88 | 4.8 | 3011 | 9 US-09-995-937-20 | Sequence 20, Appli |
| 33 | 88 | 4.8 | 3011 | 10 US-09-742-659-4 | Sequence 4, Appli |
| 34 | 88 | 4.8 | 3011 | 10 US-09-738-626-4027 | Sequence 9, Appli |
| 35 | 88 | 4.8 | 3011 | 10 US-09-952-572-9 | Sequence 2, Appli |
| 36 | 88 | 4.8 | 3012 | 9 US-09-995-937-2 | Sequence 2, Appli |
| 37 | 88 | 4.8 | 3012 | 10 US-09-238-076-2 | Sequence 164, App |
| 38 | 87.5 | 4.8 | 281 | 9 US-09-984-245-164 | Sequence 4, Appli |
| 39 | 87 | 4.8 | 3782 | 9 US-09-860-846-4 | Sequence 4, Appli |
| 40 | 87 | 4.8 | 3782 | 10 US-09-861-289-4 | Sequence 4, Appli |
| 41 | 86.5 | 4.7 | 208 | 10 US-09-921-397-93 | Sequence 93, Appli |
| 42 | 86.5 | 4.7 | 230 | 9 US-09-738-626-4027 | Sequence 4027, Ap |
| 43 | 86.5 | 4.7 | 692 | 9 US-09-738-626-6979 | Sequence 6979, Ap |
| 44 | 85.5 | 4.7 | 276 | 12 US-10-033-078-16 | Sequence 16, Appli |
| 45 | 85.5 | 4.7 | 315 | 10 US-09-815-242-11636 | Sequence 11636, A |

ALIGNMENTS

RESULT 1
US-09-779-144A-7
; Sequence 7, Application US/09779144A
; Patent No. US20020148006A1
; GENERAL INFORMATION:
; APPLICANT: Nes, David W.
; TITLE OF INVENTION: Transgenic Plants with Modified Sterol Compositions
; FILE REFERENCE: 11899, 0198, DVUS01 MOB:198
; CURRENT APPLICATION NUMBER: US/09/779,144A
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: US 09/106,926
; PRIOR FILING DATE: 1998-06-29
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Zea mays
; US-09-779-144A-7

| | | | | |
|-----------------------|-------|------------------------------------------------------------|--------|------------------------------------|
| Query Match | 12.3% | Score 225; | DB 10; | Length 344; |
| Best Local Similarity | 25.4% | Pred. No. 3.6e-14; | | |
| Matches | 77; | Conservative | 40; | Mismatches 112; Indels 74; Gaps 9; |
| QY | 69 | IAEFTDESSGLMENTWGDHMHGFFDOSGTVSLSDHRAAQMIOESLRFASVSEBRKW | 128 | |
| DB | 51 | VAKYVDLATSFEYEGWGESFHFARHNGESTLRESIKRHHFLALQGLT-----KP | 100 | |
| QY | 129 | PSIYDVGCGIGSSRYLAKFGATSV-GITLSPVQAQANLAAAGGLADKVSFOVADA | 187 | |
| DB | 101 | GKKVLDVGGIGGIGPLRELA-RFSSSVYGLNNNEYITGKELNRLAGISGCDPFAKADP | 159 | |
| QY | 188 | LOQPSDGOFDLVMSWESGEHMPDRAKEFVGEIARVAAPGAILIIVTW-----H | 236 | |
| DB | 160 | KMPFDNNTFADVAVLEACHAPDPVGCCKEILRYLPQGCRAVYEMCTDHYDPNNATH | 219 | |
| QY | 237 | R-----DLG-----PDEQSLHP-----MEQILLKRICDAVYLPAMCS----- | 268 | |
| DB | 220 | KRIKDEIEIGNGLPIRSTRQCLRAVKDAGFEVYMDKDAEDSPJWPYLPIDPSRFLSS | 279 | |
| QY | 269 | -----TSDYKILQSLSLQDKSKSDMSRFAPAFPRAVIRASFTMKGLSLSSSQ | 318 | |

Db 280 FRUTSVGRMTPTWVKALEYGLADPGSERVSSFILE-----KAAEGIVEGCK 326
 Oy 319 KTI 321
 Db 327 KEI 329

RESULT 2

US-09-779-144A-4
 ; Sequence 4, Application US/09779144A
 ; Patent No. US20020148006A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Nes, David W.
 ; TITLE OF INVENTION: Transgenic Plants with Modified Sterol Compositions
 ; FILE REFERENCE: 11899.0198. DIVS01 MOB7:198
 ; CURRENT FILING DATE: 2001-02-08
 ; CURRENT APPLICATION NUMBER: US/09/779,144A
 ; PRIOR FILING DATE: 1998-06-29
 ; PRIOR APPLICATION NUMBER: US 09/106,926
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 361
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 US-09-779-144A-4

Query Match 11.6%; Score 212.5; DB 10; Length 361;
 Best Local Similarity 25.4%; Pred. No. 6.6e-13;
 Matches 80; Conservative 54; Mismatches 144; Indels 37; Gaps 11;

Oy 55 QKPKK-DKKKKLQKGLAEFYDESSGLMENIWDHMHGFDSPSTVLSLSD-----HRAOI 109
 Db 59 RRKELETAKVDFVDFETNLVTDITWCGSGSFH--FSPSTPGSKHRTATRLHEMAY 116
 Oy 110 RMIOESLRFAVSEERSKMKPSIVDVGCGIGSSRYLAKFGATSVGITLSPVOAQRANA 169
 Db 117 DLIO-----VKPQKILIDVCGGVGPMRAIASRANVVCITINEYOVNARL 164
 Oy 170 LAAAGLADKVSFOVADALDQPPSDGOFDLYWMESEHNPDKAKFYGELARPAARPAIT 229
 Db 165 HNKAGIGDALCEYVCGFLOMPDMSFDGAYSIKATCHAPKLEEVYAEIYRLVKPGSMY 224
 Oy 230 IYTWCHRDGLPDEQSLHPMEODLKRICDAYILPAMCSTSDYKILQSLDIDKESDW 289
 Db 225 VSTEWTTEFKAEDEH---VEYIOGIERGDALPGLRAYVDIAETKAKYGFELVRKDL 281
 Oy 290 SRPVA-PFMPAVI--RSASFYWKG--LSLSLSSGOKTKGALAMPAMI-----EGYKK 336
 Db 282 ASPPAEPWMTRLKMGRLAY-WRNHIVYOILSAGVAPKGTVDVHEMLFKTADCLTRGET 340
 Oy 337 DLIK-PAIITCRKPE 350
 Db 341 GIFSPMHMILCRKPE 355

RESULT 3

US-09-801-368-96
 ; Sequence 96, Application US/09801368
 ; Patent No. US20020128250A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Busby, Robert
 ; APPLICANT: Busby, Robert
 ; APPLICANT: Hecht, Peter
 ; APPLICANT: Hecht, Peter
 ; APPLICANT: Holtzman, Doug
 ; APPLICANT: Holtzman, Doug
 ; APPLICANT: Madden, Kevin
 ; APPLICANT: Maxon, Mary
 ; APPLICANT: Milne, Todd
 ; APPLICANT: No. US20020128250A1man, Thea
 ; APPLICANT: Royer, John
 ; APPLICANT: Salama, Sofie
 ; APPLICANT: Sherman, Amir
 ; APPLICANT: Silva, Jeff

APPLICANT: Summers, Eric
 ; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fu
 ; FILE REFERENCE: 109272.147
 ; CURRENT APPLICATION NUMBER: US/09/801,368
 ; CURRENT FILING DATE: 2001-03-07
 ; PRIOR APPLICATION NUMBER: US 09/487,558
 ; PRIOR FILING DATE: 2000-01-19
 ; PRIOR APPLICATION NUMBER: US 60/160,587
 ; PRIOR FILING DATE: 1999-10-20
 ; NUMBER OF SEQ ID NOS: 440
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 96
 ; LENGTH: 383
 ; TYPE: PRT
 ; ORGANISM: Saccharomyces cerevisiae
 US-09-801-368-96

Query Match 11.1%; Score 203.5; DB 10; Length 383;
 Best Local Similarity 21.8%; Pred. No. 5.5e-12;
 Matches 78; Conservative 58; Mismatches 149; Indels 73; Gaps 12;

Oy 42 SAASERGEIVLEQKPKKDKKKLQKGLAEFYDESSGLMENI-----MGDHMHG-F 92
 Db 36 NSAKQKAVOKYLRNMDGRTDKDAEERL-EDYNEATHSYNNVTDYETGWSGSPHSRF 94
 Oy 93 YSDS---TVSLDHRRAOIRMOESLRFAVSEERSKMKPSIVDVGCGIGSSRYLAK 149
 Db 95 YKGSFASASIRHEHLYLAVKAGIORG-----DLVDVCGGVGPARETARF 140
 Oy 150 FGATSVGITLSPVOAQRANLAAAGLADKVSFOVADALDQPPSDGOFDLYWMESEHNP 209
 Db 141 TGCNIVIGLNNNDQIKAKYAKKYNLSDDMFVKGDPMDEEFTDVAIATCHA 200
 Oy 210 PDKAKFYGELARPAARPAITIIYTWCHRDGLPDEQSLHPMEODLKRICDAYI-----L 263
 Db 201 KLEGVYSEIYKVLKAGCGFAVEWMTDKYDENNEH-----KRI-AYEELGDGI 251
 Oy 264 PAMCSTSDYKILQSLDIDKESD-----WSRFVAPFMPAV-----IRSAF 305
 Db 252 PKMFHVDVAKALKKNGCFEVLVSEDLADNDEIPWYPLTGEMKYVONLANLATFFFTSY 311
 Oy 306 TWKGLSS-----LLSSGOKTKGAL--AMPLMIGYKKDLKFAIITCRKPE 350
 Db 312 LGRQFTTAMTVMEKIGLAEBSKEVYALLENAAVGLAGGSKSLFTPMILFARKPE 369

RESULT 4

US-09-779-144A-2
 ; Sequence 2, Application US/09779144A
 ; Patent No. US20020148006A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Nes, David W.
 ; TITLE OF INVENTION: Transgenic Plants with Modified Sterol Compositions
 ; FILE REFERENCE: 11899.0198. DIVS01 MOB7:198
 ; CURRENT FILING DATE: 2001-02-08
 ; CURRENT APPLICATION NUMBER: US/09/779,144A
 ; PRIOR FILING DATE: 1998-06-29
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 383
 ; TYPE: PRT
 ; ORGANISM: Saccharomyces cerevisiae
 US-09-779-144A-2

Query Match 11.1%; Score 203.5; DB 10; Length 383;
 Best Local Similarity 21.8%; Pred. No. 5.5e-12;
 Matches 78; Conservative 58; Mismatches 149; Indels 73; Gaps 12;

Oy 42 SAASERGEIVLEQKPKKDKKKLQKGLAEFYDESSGLMENI-----MGDHMHG-F 92
 Db 36 NSAKQKAVOKYLRNMDGRTDKDAEERL-EDYNEATHSYNNVTDYETGWSGSPHSRF 94

SEQ ID NO 11
LENGTH: 348
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-09-939-521-11

Query Match 5.7% Score 105; DB 10; Length 348;

Best Local Similarity 23.6%; Pred. No. 0.025; Mismatches 74; Indels 58; Gaps 12;

Matches 51; Conservative 33; Mismatches 74; Indels 58; Gaps 12;

DB 103 DHRAAQIMIDSLRFS-----VSEERSKPKSIIVDVGSGIGSSRYLAKKFGATSVGI 157

DB 28 DHYGHEEMLDGYRTLSYRNAIIONKDLFKDKIVLDVCGCTGLISMFAAKHGAHVIGV 87

DB 158 TLSPVOAQRANALAAOGLAKVSP--QVADALQPFSDQFDLYWSMESG-----EHM 209

DB 88 DMSSI-TEMKELVELNFSKIDTLRGKLED-VHLPPP--KVDIISEMNGYFLLYESM 143

DB 210 PDKKFGVGLARVAAPGAIITIVTWCNRDLGPEOSLHPMEDLLKKICDAYY---LPA 265

DB 144 MDYVLVYARD--HYLVEGGILF-----PDKCSIH-----LAGLEDSDYKDEKLVY 185

DB 266 WCSTSDYVKLQSLQSLQDISEDSRFPVAPFMPAVI 301

DB 186 W-----QDVYGGDYS---PFVPLVL 202

RESULT 14

US-09-815-242-12602

Sequence 12602, Application US/09815242

Patent No. US20020061569A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Karl L.

APPLICANT: Zyskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

TITLE OF INVENTION: Identification of Essential Genes In

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 12602

LENGTH: 241

TYPE: PRT

ORGANISM: Staphylococcus aureus

US-09-815-242-12602

Query Match 5.4% Score 99; DB 10; Length 241;

Best Local Similarity 18.6%; Pred. No. 0.058; Mismatches 108; Indels 100; Gaps 11;

Matches 58; Conservative 46; Mismatches 108; Indels 100; Gaps 11;

DB 54 EOKPKDDKKLQKIGAEFDESSGLMENIWGDHMHGFDSDSYVSLSDHRAAQIRMIQ 113

DB 114 E-SLRPASYSEERSKPKSIIVDVGSGIGSSRYLAKKFGATSV--VGITLSPVOAQRANAL 170

DB 3 DNKANKQVHRVFPONISKYDRLNNI-----ISFEQHKVVRKRYMK 43

DB 114 E-SLRPASYSEERSKPKSIIVDVGSGIGSSRYLAKKFGATSV--VGITLSPVOAQRANAL 170

DB 44 DMVGROGT-----KALDVCCGIGDWTIALSKANGPFGVYTGIDFSSNMILEYKREK 93

DB 171 AAAGLADKVSFOYADALQOFPDSDGQFDLYWSMESGEHMPKAFVGLARVAAPGAIIT 230

DB 94 TASH---ENVVLVGDAMLELPEEDNSFDYVITIGFGLRVDPYLVALKEMHRLKPGCHVY 150

DB 231 IVTWCNRDLGPEOSLHPMEDLLKKICDAYYLRWCSTSDYVKLQSLQDISEDS 290

DB 151 CLETSOPLT-----PVRKOMAYLYF----- 170

DB 291 RFVAPFMP---AVIRSAFTMGSLSSLSGQTKT-----GALAMP 329

DB 171 KFMPIFGKLFRAKSEYEMIQOSTFNPGRKELKMEFEAGFIVRVRSFTGVAAHML 230

DB 330 MIEGKY-KDLIK 340

DB 231 ---GYKENDNTR 239

RESULT 15

US-09-815-242-5314

Sequence 5314, Application US/09815242

Patent No. US20020061569A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Karl L.

APPLICANT: Zyskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

TITLE OF INVENTION: Identification of Essential Genes In

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5314

LENGTH: 234

TYPE: PRT

ORGANISM: Staphylococcus aureus

US-09-815-242-5314

Query Match 5.4% Score 98.5; DB 10; Length 234;

Best Local Similarity 20.6%; Pred. No. 0.062; Mismatches 75; Indels 35; Gaps 5;

Matches 37; Conservative 33; Mismatches 75; Indels 35; Gaps 5;

DB 54 EOKPKDDKKLQKIGAEFDESSGLMENIWGDHMHGFDSDSYVSLSDHRAAQIRMIQ 113

DB 1 DNKANKQVHRVFPONISKYDRLNNI-----ISFEQHKVVRKRYMK 41

DB 114 E-SLRPASYSEERSKPKSIIVDVGSGIGSSRYLAKKFGATSV--VGITLSPVOAQRANAL 170

Db 42 DMGVRGCT-----KALDYCCGTGDMTIALSKAVGPIGEVTCIDSENNMLEYGKEK 91
Qy 171 AAAQGLADYVSFOVADALQQPESDGGQDLVWSHESGEHMPDKAKVEYGEIARVAAPGAIIT 230
Db 92 TASM---ENVKLVHGDAMELPFEDNSFDYVTIGFGLRNVPDYLVALKEMNRVLKPGGMVY 148

Search completed: March 18, 2003, 17:42:40
Job time : 18 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 18, 2003, 17:36:22 ; Search time 19 Seconds
(Without alignments)
1770.897 Million cell updates/sec

Title: US-09-857-613A-28

Perfect score: 1830
Sequence: 1 MATVVRIPITSCIHIFRFS.....IEGKKDLIKFAITTCRKP 350

Scoring table: BLOSUM62
Gapop 10.0 , Gapect 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR_73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----------|--------------------|
| 1 | 1154.5 | 63.1 | 348 | 2 C96673 | gamma-tocopherol m |
| 2 | 659 | 36.0 | 280 | 2 AE2031 | gamma-tocopherol m |
| 3 | 647.5 | 35.4 | 317 | 2 S76618 | hypothetical prote |
| 4 | 392.5 | 21.4 | 330 | 2 AC2071 | hypothetical prote |
| 5 | 392 | 21.4 | 318 | 2 S76226 | hypothetical prote |
| 6 | 247 | 13.5 | 352 | 2 T03845 | probable sterol 24 |
| 7 | 241 | 13.2 | 363 | 2 T06795 | probable sterol 24 |
| 8 | 238 | 13.0 | 283 | 2 T44579 | C5-O-methyltransfe |
| 9 | 227 | 12.4 | 344 | 2 T04138 | sterol 24-C-methyl |
| 10 | 226 | 12.3 | 283 | 2 UC6531 | avermectin B 5-O-m |
| 11 | 225 | 12.3 | 344 | 2 T01572 | sterol 24-C-methyl |
| 12 | 221.5 | 12.1 | 357 | 2 T03848 | probable sterol 24 |
| 13 | 221.5 | 12.1 | 378 | 2 T39579 | sterol methyltrans |
| 14 | 218.5 | 11.9 | 324 | 2 T42375 | probable sterol 24 |
| 15 | 212.5 | 11.6 | 361 | 2 S63686 | sterol 24-C-methyl |
| 16 | 210 | 11.5 | 379 | 2 T50969 | probable sterol 24 |
| 17 | 204 | 11.1 | 367 | 2 T06780 | sterol 24-C-methyl |
| 18 | 203.5 | 11.1 | 383 | 1 A42003 | sterol 24-C-methyl |
| 19 | 194.5 | 10.6 | 346 | 2 T10173 | sterol 24-C-methyl |
| 20 | 190 | 10.4 | 374 | 2 T96525 | protein T1N15.23 f |
| 21 | 188 | 10.3 | 555 | 2 H96762 | hypothetical prote |
| 22 | 182 | 9.9 | 366 | 2 T33885 | hypothetical prote |
| 23 | 180 | 9.9 | 376 | 2 B70797 | probable transfera |
| 24 | 169 | 9.2 | 218 | 2 H84364 | membrane protein f |
| 25 | 164.5 | 9.0 | 394 | 2 C82951 | conserved hypothet |
| 26 | 163 | 8.9 | 437 | 2 T29330 | hypothetical prote |
| 27 | 161 | 8.8 | 387 | 2 C70549 | hypothetical prote |
| 28 | 161 | 8.8 | 387 | 2 A81324 | cyclopropane-fatty |
| 29 | 157 | 8.6 | 274 | 2 G86977 | probable methyltra |

| | | | | | |
|----|-------|-----|-----|----------|--------------------|
| 30 | 156.5 | 8.6 | 273 | 2 T34740 | hypothetical prote |
| 31 | 156 | 8.5 | 274 | 2 B70901 | hypothetical prote |
| 32 | 156 | 8.5 | 274 | 2 AF3437 | cyclopropane-fatty |
| 33 | 153.5 | 8.4 | 347 | 2 C70723 | probable methyltra |
| 34 | 153 | 8.4 | 382 | 2 AC0696 | cyclopropane-fatty |
| 35 | 152 | 8.3 | 382 | 2 A44292 | cyclopropane-fatty |
| 36 | 152 | 8.3 | 382 | 2 AG0291 | cyclopropane-fatty |
| 37 | 150 | 8.2 | 382 | 2 B90925 | cyclopropane fatty |
| 38 | 150 | 8.2 | 382 | 2 F85773 | cyclopropane fatty |
| 39 | 149 | 8.1 | 306 | 2 S18533 | eryg protein - Sac |
| 40 | 149 | 8.1 | 409 | 2 D87426 | cyclopropane-fatty |
| 41 | 148.5 | 8.1 | 278 | 2 E82965 | hypothetical prote |
| 42 | 147.5 | 8.1 | 452 | 2 B75306 | probable cyclopro |
| 43 | 146.5 | 8.0 | 389 | 2 B71865 | cyclopropane-fatty |
| 44 | 146.5 | 8.0 | 389 | 2 H64571 | cyclopropane-fatty |
| 45 | 144.5 | 7.9 | 241 | 2 C87607 | hypothetical prote |

ALIGNMENTS

RESULT 1

C96673
gamma-tocopherol methyltransferase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: C96673
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiet, N.A.; Kaul, S.; White, O.
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Cressy, T.H.; I
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maitl, R.;
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Ventler, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: C96673
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-348 <STO>
A:Cross-references: GB:AE005173; NID:98099780; PIDN:AAD38271.2; GSPDB:GNO0141
C:Genetics:
A:Gene: F13011.27
A:Map position: 1

Query Match 63.1%; Score 1154.5; DB 2; Length 348;
Best Local Similarity 69.4%; Pred. No. 3e-87;
Matches 227; Conservative 28; Mismatches 61; Indels 11; Gaps 4

| | | |
|----|-----|-----------------------------------------------------------------|
| QY | 32 | GPRSWAPIRASAAASE-----RGEIVLEQPKKDDKKLOKIAEFGDESSGLMWNIG 85 |
| DB | 23 | GSKSLIFRSPSSSSSMWTGNAVAAATSTE--ALRKIAEYNTSLMEIING 80 |
| QY | 86 | DHHHGFEYDSDFVSLSDD--HRAAOIRMOIESLRFASVS--EERSKPKSIVDVGCGIGS 142 |
| DB | 81 | DHHHGFEYDSSVQSLDSGSHKKAQIRMEDESIRFGAYNDEEEKIKKKVVDVGGCGIGS 140 |
| QY | 143 | SRYLAKFGATVGYTLSPVQAOANALAAAGLADKVSQVADALQOPSSDGFVLVMS 202 |
| DB | 141 | SRYLAKFGAECIGITLSPVQAKRANDLAQAOSLAHKAASFQVADALQOPEDGFFDLVMS 200 |
| QY | 203 | MESGEHMPDKAKVGVGLARAAAGATITITWCHROLDGPRDOSLHPEDOLKKICDAY 262 |
| DB | 201 | MESGEHMPDKAKFVKELVRAAPGRITITWCHRNLSAGEEALQPEQNLIDKICTFY 260 |
| QY | 263 | LPAMCSTDDVYVVKLQSLQSDIKSEDMRSFVAPFPVAFVSAFTWKLSSLLSSGOKTK 322 |
| DB | 261 | LPAMCSTDDVYVVKLQSLQSDIKCAQMSSENVAPFPVAFVITATLWKLVLSSRGMMSIK 320 |
| QY | 323 | GALAMPILIEGKKDLIKFAITTCRKP 349 |
| DB | 323 | GALAMPILIEGKKDLIKFAITTCRKP 349 |

Db 321 GATMLPMIMEGYKGVKRGITTCQKP 347

RESULT 2

AE2031
gamma-tocopherol methyltransferase (imported) - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp.

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002

C:Accession: AE2031

R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena Res. 8, 205-213, 2001

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AE2031

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-280 <KUR>

A:Cross-references: GB:BA000019; PIDN:BA073502.1; PID:g17130893; GSPDB:GN00179

A:Experimental source: strain PCC 7120

A:Gene: alr1803

Query Match

Best Local Similarity 36.0%; Score 659; DB 2; Length 280;

Matches 138; Conservative 42; Mismatches 92; Indels 8; Gaps 3;

QY 65 LOKGIAEFYDESSGLWENIMGDHMHGFYDSSTVSLSDHRAOIRMIQESLRFASVSEE 124

Db 5 LYQOIQOFPYDASSSGIMEITWSEHMHGYYGADGT-EQKNRQAOIDLIELLTWAGV--- 60

QY 125 RSKMPKSIYDVCGGIGSSRYLAKFKGATSVGITLSPVOAQRANALAAAGLADVSFOY 184

Db 61 --QTAENLIDYCGGIGSSRYLAKFKGATSVGITLSPVOAQRANALAAAGLADVSFOY 118

QY 185 ADALQOFPSPDGFPLVWMSGEHMPDKAKFVGLARVAPGAIITVWCHRDLPDEQ 244

Db 119 ANAQAMPFDDNSFDLWVMSGEHMPDKAKFVGLARVAPGAIITVWCHRDLPDEQ 176

QY 245 SLHPWEDLLKIKIDAVYLPAMCSTSDYVKLQSLSDIKSEDSMRFAVPFVAVIRSA 304

Db 177 PLTADERRHLQAIYDYCLPYVSLPDYAIARECGFGELKTRADMSVAVAPFVAVIRSA 236

QY 305 FTWKGLSSLSGQRTIKGALAMPIMEGYKKDLIKFAITTCRKP 349

Db 237 FTPOAIRFGLRACGWTITGALISGLMRGGERGLIRFGL 276

QY 305 FTWKGLSSLSGQRTIKGALAMPIMEGYKKDLIKFAITTCRKP 349

Db 237 FTPOAIRFGLRACGWTITGALISGLMRGGERGLIRFGL 276

QY 305 FTWKGLSSLSGQRTIKGALAMPIMEGYKKDLIKFAITTCRKP 349

Db 237 FTPOAIRFGLRACGWTITGALISGLMRGGERGLIRFGL 276

QY 305 FTWKGLSSLSGQRTIKGALAMPIMEGYKKDLIKFAITTCRKP 349

Db 237 FTPOAIRFGLRACGWTITGALISGLMRGGERGLIRFGL 276

QY 305 FTWKGLSSLSGQRTIKGALAMPIMEGYKKDLIKFAITTCRKP 349

Db 237 FTPOAIRFGLRACGWTITGALISGLMRGGERGLIRFGL 276

QY 305 FTWKGLSSLSGQRTIKGALAMPIMEGYKKDLIKFAITTCRKP 349

Db 237 FTPOAIRFGLRACGWTITGALISGLMRGGERGLIRFGL 276

QY 305 FTWKGLSSLSGQRTIKGALAMPIMEGYKKDLIKFAITTCRKP 349

Db 237 FTPOAIRFGLRACGWTITGALISGLMRGGERGLIRFGL 276

QY 305 FTWKGLSSLSGQRTIKGALAMPIMEGYKKDLIKFAITTCRKP 349

Db 237 FTPOAIRFGLRACGWTITGALISGLMRGGERGLIRFGL 276

QY 305 FTWKGLSSLSGQRTIKGALAMPIMEGYKKDLIKFAITTCRKP 349

Db 237 FTPOAIRFGLRACGWTITGALISGLMRGGERGLIRFGL 276

QY 305 FTWKGLSSLSGQRTIKGALAMPIMEGYKKDLIKFAITTCRKP 349

Db 237 FTPOAIRFGLRACGWTITGALISGLMRGGERGLIRFGL 276

QY 305 FTWKGLSSLSGQRTIKGALAMPIMEGYKKDLIKFAITTCRKP 349

Db 237 FTPOAIRFGLRACGWTITGALISGLMRGGERGLIRFGL 276

QY 305 FTWKGLSSLSGQRTIKGALAMPIMEGYKKDLIKFAITTCRKP 349

Matches 135; Conservative 45; Mismatches 102; Indels 3; Gaps 3;

QY 65 LOKGIAEFYDESSGLWENIMGDHMHGFYDSSTVSLSDHRAOIRMIQESLRFASVSEE 124

Db 34 LYKIKINFYDSSGGLWEDVGEHMHGYYGADGT-EQKNRQAOIDLIELLTWAGV--- 60

QY 125 RSKMPKSIYDVCGGIGSSRYLAKFKGATSVGITLSPVOAQRANALAAAGLADVSFOY 184

Db 92 SAK-PKRIIDLCGGIGSSRYLAKFKGATSVGITLSPVOAQRANALAAAGLADVSFOY 150

QY 185 ADALQOFPSPDGFPLVWMSGEHMPDKAKFVGLARVAPGAIITVWCHRDLPDEQ 244

Db 151 ANAQAMPFDDNSFDLWVMSGEHMPDKAKFVGLARVAPGAIITVWCHRDLPDEQ 176

QY 245 SLHPWEDLLKIKIDAVYLPAMCSTSDYVKLQSLSDIKSEDSMRFAVPFVAVIRSA 304

Db 211 PLTADERRHLQAIYDYCLPYVSLPDYAIARECGFGELKTRADMSVAVAPFVAVIRSA 236

QY 305 FTWKGLSSLSGQRTIKGALAMPIMEGYKKDLIKFAITTCRKP 349

Db 271 FDPRLVLMALGQAGPKIINNALCLRLMKWCEGVLRFGLTQIKP 315

QY 305 FTWKGLSSLSGQRTIKGALAMPIMEGYKKDLIKFAITTCRKP 349

Db 271 FDPRLVLMALGQAGPKIINNALCLRLMKWCEGVLRFGLTQIKP 315

QY 305 FTWKGLSSLSGQRTIKGALAMPIMEGYKKDLIKFAITTCRKP 349

Db 271 FDPRLVLMALGQAGPKIINNALCLRLMKWCEGVLRFGLTQIKP 315

QY 305 FTWKGLSSLSGQRTIKGALAMPIMEGYKKDLIKFAITTCRKP 349

Db 271 FDPRLVLMALGQAGPKIINNALCLRLMKWCEGVLRFGLTQIKP 315

QY 305 FTWKGLSSLSGQRTIKGALAMPIMEGYKKDLIKFAITTCRKP 349

Db 271 FDPRLVLMALGQAGPKIINNALCLRLMKWCEGVLRFGLTQIKP 315

QY 305 FTWKGLSSLSGQRTIKGALAMPIMEGYKKDLIKFAITTCRKP 349

Db 271 FDPRLVLMALGQAGPKIINNALCLRLMKWCEGVLRFGLTQIKP 315

QY 305 FTWKGLSSLSGQRTIKGALAMPIMEGYKKDLIKFAITTCRKP 349

Db 271 FDPRLVLMALGQAGPKIINNALCLRLMKWCEGVLRFGLTQIKP 315

QY 305 FTWKGLSSLSGQRTIKGALAMPIMEGYKKDLIKFAITTCRKP 349

Db 271 FDPRLVLMALGQAGPKIINNALCLRLMKWCEGVLRFGLTQIKP 315

QY 305 FTWKGLSSLSGQRTIKGALAMPIMEGYKKDLIKFAITTCRKP 349

Db 271 FDPRLVLMALGQAGPKIINNALCLRLMKWCEGVLRFGLTQIKP 315

QY 305 FTWKGLSSLSGQRTIKGALAMPIMEGYKKDLIKFAITTCRKP 349

Db 271 FDPRLVLMALGQAGPKIINNALCLRLMKWCEGVLRFGLTQIKP 315

QY 305 FTWKGLSSLSGQRTIKGALAMPIMEGYKKDLIKFAITTCRKP 349

Db 271 FDPRLVLMALGQAGPKIINNALCLRLMKWCEGVLRFGLTQIKP 315

QY 305 FTWKGLSSLSGQRTIKGALAMPIMEGYKKDLIKFAITTCRKP 349

Db 271 FDPRLVLMALGQAGPKIINNALCLRLMKWCEGVLRFGLTQIKP 315

QY 305 FTWKGLSSLSGQRTIKGALAMPIMEGYKKDLIKFAITTCRKP 349

Db 271 FDPRLVLMALGQAGPKIINNALCLRLMKWCEGVLRFGLTQIKP 315

QY 305 FTWKGLSSLSGQRTIKGALAMPIMEGYKKDLIKFAITTCRKP 349

Db 271 FDPRLVLMALGQAGPKIINNALCLRLMKWCEGVLRFGLTQIKP 315

QY 305 FTWKGLSSLSGQRTIKGALAMPIMEGYKKDLIKFAITTCRKP 349

Db 271 FDPRLVLMALGQAGPKIINNALCLRLMKWCEGVLRFGLTQIKP 315

QY 305 FTWKGLSSLSGQRTIKGALAMPIMEGYKKDLIKFAITTCRKP 349

Db 271 FDPRLVLMALGQAGPKIINNALCLRLMKWCEGVLRFGLTQIKP 315

QY 305 FTWKGLSSLSGQRTIKGALAMPIMEGYKKDLIKFAITTCRKP 349

Db 271 FDPRLVLMALGQAGPKIINNALCLRLMKWCEGVLRFGLTQIKP 315

QY 305 FTWKGLSSLSGQRTIKGALAMPIMEGYKKDLIKFAITTCRKP 349

Db 271 FDPRLVLMALGQAGPKIINNALCLRLMKWCEGVLRFGLTQIKP 315

QY 305 FTWKGLSSLSGQRTIKGALAMPIMEGYKKDLIKFAITTCRKP 349

Db 271 FDPRLVLMALGQAGPKIINNALCLRLMKWCEGVLRFGLTQIKP 315

QY 305 FTWKGLSSLSGQRTIKGALAMPIMEGYKKDLIKFAITTCRKP 349

Db 271 FDPRLVLMALGQAGPKIINNALCLRLMKWCEGVLRFGLTQIKP 315

QY 305 FTWKGLSSLSGQRTIKGALAMPIMEGYKKDLIKFAITTCRKP 349

Db 271 FDPRLVLMALGQAGPKIINNALCLRLMKWCEGVLRFGLTQIKP 315

QY 305 FTWKGLSSLSGQRTIKGALAMPIMEGYKKDLIKFAITTCRKP 349

RESULT 8

T44579

C5-O-methyltransferase [imported] - Streptomyces avermectilis

C:Species: Streptomyces avermectilis

C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000

C:Accession: T44579

R:Ikeda, H.; Nonomiya, T.; Usami, M.; Ohta, T.; Omura, S.

Proc. Natl. Acad. Sci. U.S.A. 96, 9509-9514, 1999

A:Title: Organization of the biosynthetic gene cluster for the polyketide anthelmintic m

A:Reference number: 222796; MUID:99380548; PMID:10449723

A:Accession: T44579

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-283 <IKE>

A:Cross-references: EMBL:AB032524; NID:g5921164; PIDN:BAAB4602.1; PID:g5921167

C:Genetics:

A:Note: aved

Query Match

Best Local Similarity 26.3%, Score 238; DB 2; Length 283;

Matches 80; Conservative 51; Mismatches 135; Indels 38; Gaps 10;

Qy 57 PKDDKKRLQKIAEFYDESSGLMWNHGFYDSSTVSLSDHRAAQIRMIOESL 116

Db 5 PEQTPPSLEVG--DYDRLTDLNMRALGNTHLGYWPOPGDS--SPGKAA-----DRL 55

Qy 117 RFASVSEERSKMPKSIYVCGGIGSSRYLAKKRGATSVGITLSFVQAQRANALAAAGL 176

Db 56 TDLLGLKRLGITGRVRLVCGGSGKPAVRLASAPVDVGVGVSEVQGLATLAKOSH 115

Qy 177 ADKVSFOVADALQOPFSGDFDLVMSMEGEMHPDKAFVGLAVARAGAIITIVMCH 236

Db 116 ADKVVFTPADAHLELFPFGSGFDAMALCLLHNSPAOYIEIANVLRPGRLAVTDVAL 175

Qy 237 RDLGPDEQSLHPWEODLLKIKCDAYVLPAMCSTSDYVKLQSLSDIKSED--NSRFVAP 295

Db 176 RAFGTGKMKRGECTSLLA-----VPALVHIDEYACIMADAGLELHEDLDIGQVVP 228

Qy 296 FMPAV-----IRSAFTWKGLSLSSGOKTIRKALAMPIMIEGKKDLIKFAIT 345

Db 229 SFALRDHVNHEHDEYAAAF--GIG--VAEMRKVVAOCTTLP-----WTFD-IGYVVL 277

Qy 346 CRKP 349

Db 278 ARRP 281

RESULT 9

T04138

sterol 24-C-methyltransferase (EC 2.1.1.41) ESM1, endosperm - maize

N:Alternate names: C-24 sterol methyltransferase

C:Species: Zea mays (maize)

C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 03-Jun-2002

C:Accession: T04138

R:Grebencok, R.J.; Galbraith, D.W.; Dellapenna, D.

Plant Mol. Biol. 34, 891-896, 1997

A:Title: Characterization of zea-mays endosperm C-24 sterol methyltransferase - one of 2

A:Reference number: 209668; MUID:97435974; PMID:9290641

A:Accession: T04138

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-344 <GRE>

A:Cross-references: EMBL:U79669; NID:g1899059; PIDN:AA070886.1; PID:g1899060

A:Experimental source: endosperm

C:Genetics:

A:Gene: ESM1

A:Function:

A:Description: methyltransferase

C:Superfamily: 24-sterol C-methyltransferase: bioc homology

C:Keywords: methyltransferase; S-adenosylmethionine

F:101-205/Domain: bioc homology <BIOC>

Query Match

Best Local Similarity 12.4%, Score 227; DB 2; Length 344;

Best Local Similarity 24.6%, Pred. No. 5.6e-11; Matches 82; Conservative 47; Mismatches 109; Indels 96; Gaps 12;

Qy 69 IAEFYDESSGLMWNHGFYDSSTVSLSDHRAAQIRMIOESLRFASVSEERSK 128

Db 51 VNKYDALTATSEFYEGMGCSFHFARHMGESLRESIKRHEHFLAOLGL-----KP 100

Qy 129 PKSTVDCCGIGGSSRYLAKKRGATSV--GITLSFVQAQRANALAAAGLADKVSFOVADA 187

Db 101 GKNVYDVCGIGGGRLETA--RFSSTSVGLNNNEQITRGELNLAIGSTCDFKADF 159

Qy 188 LQOPFSDQFDLWMSMEGEMHPDKAFVGLAVARAGAIITIVMCH-----H 236

Db 160 MKMFPDDWTFPAVVAIEATCPADPDVCGCYKEIRLAKGCGCFAYEMKITDHYDPNMT 219

Qy 237 R-----DLG---PDEQSLHP-----WEODLLKIKCDAYVLPAMCS----- 268

Db 220 KRKDEIELGNLPDIRSTROCLQAVKDAGEVWVDKDLAEDSLPMLYLPIDPSRFSLS 279

Qy 269 -----TSDYKLLQSLSDIKSEDMSRFAPRPVAVIRSAFTWKGLSLSSGO 318

Db 280 FRLTSVGRNITRTWVKALEYGLAPQSGSERVSNFL-----E 315

Qy 319 KTIKALAMPIMIEGKKDL--IKFAITCRKP 349

Db 316 KAAEC-----LVEGKKEIFTPMVFPLV--RKP 341

RESULT 10

JC6531

avermectin B 5-O-methyltransferase (EC 2.1.1.-) - Streptomyces "avermectilis"

C:Species: Streptomyces "avermectilis"

C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 16-Jul-1999

C:Accession: JC6531

R:Ikeda, H.; Wang, L.R.; Ohta, T.; Inokoshi, J.; Omura, S.

Gene 206, 175-180, 1998

A:Title: Cloning of the gene encoding avermectin B 5-O-methyltransferase in averm

A:Reference number: JC6531; MUID:98137789; PMID:9469930

A:Accession: JC6531

A:Molecule type: DNA

A:Residues: 1-283 <IKE>

A:Experimental source: wild type K139

C:Comment: This enzyme catalyzes the methylation of the hydroxyl group at the C5

C:Genetics:

A:Gene: aved

C:Superfamily: bioc homology

C:Keywords: methyltransferase

F:68-172/Domain: bioc homology <BIOC>

Query Match

Best Local Similarity 12.3%, Score 226; DB 2; Length 283;

Matches 79; Conservative 50; Mismatches 137; Indels 38; Gaps 10;

Qy 57 PKDDKKRLQKIAEFYDESSGLMWNHGFYDSSTVSLSDHRAAQIRMIOESL 116

Db 5 PEQTPPSLEVG--DYDRLTDLNMRALGNTHLGYWPOPGDS--SPGKAA-----DRL 55

Qy 117 RFASVSEERSKMPKSIYVCGGIGSSRYLAKKRGATSVGITLSFVQAQRANALAAAGL 176

Db 56 TDLLGLKRLGITGRVRLVCGGSGKPAVRLASAPVDVGVGVSEVQGLATLAKOSH 115

Qy 177 ADKVSFOVADALQOPFSGDFDLVMSMEGEMHPDKAFVGLAVARAGAIITIVMCH 236

Db 116 ADKVVFTPADAHLELFPFGSGFDAMALCLLHNSPAOYIEIANVLRPGRLAVTDVAL 175

Qy 237 RDLGPDEQSLHPWEODLLKIKCDAYVLPAMCSTSDYVKLQSLSDIKSED--NSRFVAP 295

Db 176 RAFGTGKMKRGECTSLLA-----VPALVHIDEYACIMADAGLELHEDLDIGQVVP 228

Qy 296 FMPAV-----IRSAFTWKGLSLSSGOKTIRKALAMPIMIEGKKDLIKFAIT 345

Db 229 SFALRDHVNHEHDEYAAAF--GIG--VAEMRKVVAOCTTLP-----WTFD-IGYVVL 277

A: Experimental source: strain xanthi line S16; tissue-type calli from protoplasts
C: Superfamily: 24-sterol C-methyltransferase; bioc homology

Db 185 HMPFEDNTFDYVVAIEATVHAPSLSEGVGEIFRLKPGCVFQVY

QY 249 WEQDLKKICDAYLLPWCSTSDYVKLLQSLSLQDIKSED 286

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 18, 2003, 17:36:22 ; Search time 11 Seconds

(without alignments)
1319.701 Million cell updates/sec

Title: US-09-857-613A-28

Perfect score: 1830

Sequence: 1 MATVVRIPRTSCIHIFRS.....IEGKKDLIFALITCKPE 350

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Swissprot_40:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length DB | ID | Description |
|------------|-------|-------------|-----------|----|-------------|
| 1 | 221.5 | 12.1 | 378 | 1 | ERG6_SCHPO |
| 2 | 203.5 | 11.1 | 382 | 1 | ERG6_YEAST |
| 3 | 189 | 10.3 | 376 | 1 | ERG6_CANAL |
| 4 | 174 | 9.5 | 394 | 1 | YLP3_PSEPU |
| 5 | 156 | 8.5 | 274 | 1 | YEO5_MYCTU |
| 6 | 152 | 8.3 | 381 | 1 | CFA_ECOLI |
| 7 | 143 | 7.8 | 251 | 1 | BIOC_ERWHE |
| 8 | 141 | 7.7 | 251 | 1 | Y095_HARTN |
| 9 | 137 | 7.5 | 238 | 1 | UBIG_RALSO |
| 10 | 134.5 | 7.3 | 242 | 1 | UBIG_PASNU |
| 11 | 131.5 | 7.2 | 289 | 1 | UBIG_NEIMB |
| 12 | 131.5 | 7.2 | 289 | 1 | UBIG_RICCN |
| 13 | 130 | 7.1 | 274 | 1 | YEO3_MYCTU |
| 14 | 129.5 | 7.1 | 238 | 1 | UBIG_NEIMA |
| 15 | 128 | 7.0 | 232 | 1 | UBIG_PSENE |
| 16 | 125.5 | 6.9 | 244 | 1 | YXBB_BACSU |
| 17 | 124.5 | 6.8 | 240 | 1 | UBIG_ECO57 |
| 18 | 124.5 | 6.8 | 252 | 1 | UBIG_CACOR |
| 19 | 123.5 | 6.7 | 240 | 1 | UBIG_ECOLI |
| 20 | 121.5 | 6.6 | 258 | 1 | TAM_DEIRA |
| 21 | 118.5 | 6.5 | 248 | 1 | UBIG_RHIME |
| 22 | 117 | 6.4 | 242 | 1 | UBIG_YERPE |
| 23 | 117 | 6.4 | 252 | 1 | UBIG_RICPR |
| 24 | 117 | 6.4 | 257 | 1 | YIG4_YEAST |
| 25 | 116 | 6.3 | 203 | 1 | PMTA_RHOSH |
| 26 | 115.5 | 6.3 | 242 | 1 | UBIG_SALTY |
| 27 | 115.5 | 6.3 | 242 | 1 | UBIG_SALTY |
| 28 | 115.5 | 6.3 | 269 | 1 | RMMA_ECOLI |
| 29 | 115 | 6.3 | 220 | 1 | YAT1_SYNP6 |
| 30 | 113.5 | 6.2 | 417 | 1 | Y829_SYNP6 |
| 31 | 113 | 6.2 | 212 | 1 | UBIG_XYLFA |
| 32 | 111 | 6.1 | 246 | 1 | UBIG_XYLFA |
| 33 | 110 | 6.0 | 245 | 1 | UBIG_VIBCH |

ALIGNMENTS

| RESULT 1 | ID | ERG6_SCHPO | STANDARD: | PRT: | 378 AA. |
|----------|------------------------------------------------------------------------|-----------------------------------|-----------|------|---------|
| AC | 014321 | P78782 | | | |
| DT | 15-JUL-1999 | (Rel. 38, Created) | | | |
| DT | 15-JUL-1999 | (Rel. 38, Last sequence update) | | | |
| DT | 15-JUN-2002 | (Rel. 41, Last annotation update) | | | |
| DE | Probable delta(24)-sterol C-methyltransferase (EC 2.1.1.41). | | | | |
| CN | SPC169.05. | | | | |
| OC | Schizosaccharomyces pombe (fission yeast). | | | | |
| OC | Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; | | | | |
| OC | Schizosaccharomycetales; Schizosaccharomycetaceae; | | | | |
| OX | NCBI_TaxID=4896; | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN=972; | | | | |
| RX | MEDLINE=21848401; PubMed=11859360; | | | | |
| RA | Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., | | | | |
| RA | Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., | | | | |
| RA | Brooks K., Brown D., Brown S., Chillingworth J., Churcher C.M., | | | | |
| RA | Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A., | | | | |
| RA | Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., | | | | |
| RA | Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K., | | | | |
| RA | James K., Jones L., Jones M., Leather S., McDonald S., McLean J., | | | | |
| RA | Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., | | | | |
| RA | Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E., | | | | |
| RA | Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., | | | | |
| RA | Skellton J., Simmonds M., Squares R., Squares S., Stevens K., | | | | |
| RA | Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., | | | | |
| RA | Woodward J., Voiclaert G., Aert R., Robben J., Grymoperez B., | | | | |
| RA | Weldjens J., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., | | | | |
| RA | Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H., | | | | |
| RA | Borzum K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M., | | | | |
| RA | Eger P., Zimmermann M., Wedler H., Wambutt R., Purnelle B., | | | | |
| RA | Goffeau A., Cadieu E., Dreano S., Gloux S., Leclerc V., Motier S., | | | | |
| RA | Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., | | | | |
| RA | Lucas M., Rochet M., Galliard C., Tallada V.A., Garçon A., Thode G., | | | | |
| RA | Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., | | | | |
| RA | Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., | | | | |
| RA | Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., | | | | |
| RA | Shpakowski G.V., Ussery D., Barrett B.G., Nurse P., | | | | |
| RT | "The genome sequence of Schizosaccharomyces pombe."; | | | | |
| RL | Nature 415:871-880(2002). | | | | |
| RN | [2] | | | | |
| RP | SEQUENCE OF 55-378 FROM N.A. | | | | |
| RC | STRAIN=PR745; | | | | |
| RX | MEDLINE=98162722; PubMed=9501991; | | | | |
| RA | Yoshida S., Kato K., Nakai K., Okayama H., Nojima H.; | | | | |
| RT | "Identification of open reading frames in Schizosaccharomyces pombe | | | | |
| RT | CDNAS."; | | | | |
| RT | DNA Res. 4:363-369(1997). | | | | |
| CC | -I- FUNCTION: METHYLTRANSFERASE REQUIRED FOR ERGOSTEROL SYNTHESIS (BY | | | | |
| CC | STIMULATORY). | | | | |
| CC | -I- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 5-alpha-cholest- | | | | |
| CC | 8,24-dien-3-beta-ol -> S-adenosyl-L-homocysteine + 24-methylene-5- | | | | |

| | | | | | | |
|----|-------|-----|-----|---|-------------|--------------------|
| 34 | 110 | 6.0 | 296 | 1 | PRMA_HAEIN | P44402 haemophilus |
| 35 | 110 | 6.0 | 322 | 1 | COO3_ARATH | O49354 a hexapreny |
| 36 | 107.5 | 5.9 | 248 | 1 | UBIG_BRUME | O8Y198 brucella me |
| 37 | 107.5 | 5.9 | 261 | 1 | TAM_MYCTU | O33698 mycobacteri |
| 38 | 105 | 5.7 | 224 | 1 | BCWM_RHOCA | P26236 rhodobacter |
| 39 | 105 | 5.7 | 348 | 1 | HMT1_YEAST | P38074 saccharomyc |
| 40 | 104.5 | 5.7 | 249 | 1 | UBIG_RHILLO | O98987 rhizobium 1 |
| 41 | 104 | 5.7 | 248 | 1 | UBIE_RICCN | O92945 rickettsia |
| 42 | 102.5 | 5.6 | 255 | 1 | TAM_BRUME | O8Y191 brucella me |
| 43 | 101 | 5.5 | 252 | 1 | GRCB_LACIA | P49016 lactococcus |
| 44 | 100.5 | 5.5 | 251 | 1 | BIOC_ECOLI | P12999 escherichia |
| 45 | 100.5 | 5.5 | 286 | 1 | COO3_RAT | O63159 r hexapreny |

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CC      alpha-cholest-8-en-3-beta-ol.
CC      -----
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CC      -----
DR      EMBL; Z99759; CAB16897.1; -
DR      EMBL; D89131; BAA13793.1; -
DR      InterPro: IPR001601; Methyltransf.
DR      InterPro: IPR000051; SAM bind.
DR      InterPro: IPR004033; UbiE/COQ5_Metrf.
DR      Pfam; PF01209; UbiE_methyltran; 1.
KM      Sterol biosynthesis; Transferase; Methyltransferase.
FT      CONFLICT 55 63 NHEMSESD -> SVPGDPLPS (IN REF. 2).
SQ      SEQUENCE 378 AA; 42867 MW; FA4D3D82A1CE03D6 CRC64;

Query Match          12.1%; Score 221.5; DB 1; Length 378;
Best Local Similarity 22.5%; Pred. No. 3.4e-11;
Matches 63; Conservative 46; Mismatches 124; Indels 47; Gaps 5;

OY      39 IRASASSEGEIVLEOKPKDKKKLQK-----GIAEF 72
DB      19 LHGKAEEKKTGLAATASKVDQSKRLQEFEFMDRNHNESEEDRARIDGKSVNXY 78
OY      73 YDESGLEWNTWGDHMHG-PYDSDS--TVSLSDHRAAQIMIOESLRFASVSEBSK 128
DB      79 YDLADLLEYGMSQSFHSFYKGAFAQSIARHEHYLAIRMGIRKPSR----- 127
OY      129 PPSIVDVGCGIGSSRYLAKKFGATSVGTTLSPVQAORANALAAOGLADKVSFOVADL 188
DB      128 ---VLDVCGVGCPAREITEFTGICNLVGLNNNDYQISRCNNAYVRNLDKKVFKGDPW 184
OY      189 OQPFSDGQFDLWMSGESGEMPDKAFYGEELARVAAPGAIITITWCHRDGLGPDOSLHP 248
DB      185 HHPFEDNPFDYVYAEATFVHAPSLGCVGEIFRVLKPGCVFVYEMVMSD---DYDSISP 241
OY      249 WEODLLKRICDAVYILPAMKSTSDYKRLQSLSDIKSD 288
DB      242 KHREIAYNIEVGDGIPQVNRKCDAVEAIKKVGNLLEED 281

RESULT 2
ERG6_YEAST          STANDARD:          PRT:          382 AA.
AC      P25087;
DT      01-MAY-1992 (Rel. 22, Created)
DT      01-OCT-1994 (Rel. 30, Last sequence update)
DT      01-OCT-1996 (Rel. 34, Last annotation update)
DE      Delta(24)-sterol C-methyltransferase (EC 2.1.1.41).
GN      ERG6 OR SED6 OR ISE1 OR LIS1 OR YML008C OR YM9571.10C.
OS      Saccharomyces cerevisiae (Baker's yeast).
OC      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC      Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX      NCBI_TaxID=4932;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=94262330; PubMed=8203167;
RA      Hardwick K.G., Pelham H.R.B.;
RT      "SED6 is identical to ERG6, and encodes a putative methyltransferase
RT      required for ergosterol synthesis.";
RL      Yeast 10:265-269(1994).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=94312403; PubMed=8038180;
RA      Wellhinda A.A., Pavis A.D., Trumbly R.J.;
RT      "Mutations in ... (ERG6) gene confer increased sodium and lithium
RT      uptake in Saccharomyces cerevisiae.";
RL      Biochim. Biophys. Acta 1193:107-117(1994).
RN      [3]

```

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RP      SEQUENCE FROM N.A.
RC      STRAIN=S288c / AB972;
RA      Gentles S., Bowman S., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL      Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN      [4]
RP      SEQUENCE OF 1-257 FROM N.A.
RX      MEDLINE=91285426; PubMed=2060792;
RA      Hussain M., Lenard J.;
RT      "Characterization of PDR4, a Saccharomyces cerevisiae gene that
RT      confers pleiotropic drug resistance in high-copy number: identity
RT      with YAP1, encoding a transcriptional activator.";
RL      Gene 101:149-152(1991).
RN      [5]
RP      ACETYLATION.
RA      Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,
RA      Volpe T., Warner J.R., McLaughlin C.S.;
RL      Submitted (SEP-1994) to the SWISS-PROT data bank.
CC      -1- FUNCTION: METHYLTRANSFERASE REQUIRED FOR ERGOSTEROL SYNTHESIS.
CC      -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 5-alpha-cholest-
CC      8,24-dien-3-beta-ol -> S-adenosyl-L-homocysteine + 24-methylene-5-
CC      alpha-cholest-8-en-3-beta-ol.
CC      -----
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CC      or send an email to license@sib-sib.ch).
CC      -----
DR      EMBL; X74249; CAA52308.1; -
DR      EMBL; S72460; AAB31378.1; -
DR      EMBL; Z49810; CAA89944.1; -
DR      EMBL; X53830; CAA37826.1; -
DR      PIR; PE0402; PE0402.
DR      PIR; S17001; S17001.
DR      PIR; S35982; S35982.
DR      PIR; S42003; S42003.
DR      SWISS-2DPAGE; P25087; YEAST.
DR      SGD; S0004467; ERG6.
DR      InterPro: IPR001601; Methyltransf.
DR      InterPro: IPR000051; SAM bind.
KM      Sterol biosynthesis; Transferase; Methyltransferase; Acetylation.
FT      INIT MET 0 0
FT      MOD_RES 1 1 ACETYLATION.
FT      CONFLICT 379 379 E -> EE (IN REF. 2).
SQ      SEQUENCE 382 AA; 43299 MW; D76BA9E3D9CD71B CRC64;

Query Match          11.1%; Score 203.5; DB 1; Length 382;
Best Local Similarity 21.8%; Pred. No. 1.1e-09;
Matches 78; Conservative 58; Mismatches 149; Indels 73; Gaps 12;

OY      42 SAASSEGEIVLEOKPKDKKKLQKGLAEFDESSGLMNT-----WCDHMHG-F 92
DB      35 NSAQKEAVQKYLRNMDGRDKDAEERRL-EDYNEATHSYNNVTDFYEGEGSSHFHSRF 93
OY      93 YDSDS---TVSLSDHRAAQIMIOESLRFASVSEBSKWPKSIYDVCGIGSSRYLAKK 149
DB      94 YKGESEFASINRHEHYLAIRMGIRKPSR-----DVLVDGCGVGCPAREIARF 139
OY      150 FGATSVGTTLSPVQAORANALAAOGLADKVSFOVADALQPFSGQFDLWMSGESGEM 209
DB      140 TGCNVIAGLNNDYQIAKAKYKYNLSQMDFFVGDPMKMDFEENFDKVAIETATCHA 199
OY      210 PDKAFVGEELARVAAPGAIITITWCHRDGLGPDOSLHPWEDLLKIKICDAVY-----L 263
DB      200 PKLEGVSEITVVKLPKPGTFAYEVMVTKDYDENPHEH-----RKI--AEIELGGCI 250
OY      264 PFWCSTSDYVKLLQSLSDIKSD-----NSRFVAPFMPAV-----IRSAF 305
DB      251 PMFHVDAKRAKLNKCGFVLVSEDLADNDEIPIVYPLTGEMKAYVQMLANLATPFRFYS 310
OY      306 TWKGLSS-----LLSGQKTIKGL--AMPLEIIEGKKDLIFALITCKRPE 350

```

Db 311 LGRFTNATYMEKLGLEPGSKVEYALLENAAVGLVAGCKSLFTPMPLFARKPE 368

RESULT 3

ERG6 CANAL STANDARD; PRT; 376 AA.

AC 074198;

DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DE Delta(24)-sterol C-methyltransferase (EC 2.1.1.41).

GN ERG6

OS Candida albicans (Yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; mitosporic Saccharomycetales; Candida.

NCBI_TaxID=5476;

RM [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-98253976; PubMed-9593144;

RA Jensen-Pergakes K.L., Kennedy M.A., Lees N.D., Barbuch R., Koegeel C.,

RA Bard M.;

RT "Sequencing, disruption, and characterization of the Candida albicans

sterol methyltransferase (ERG6) gene: drug susceptibility studies in

erg6 mutants"; Agents Chemother. 42:1160-1167(1998).

RL Anticrib. Agents Chemother. 42:1160-1167(1998).

CC -1- FUNCTION: METHYLTRANSFERASE REQUIRED FOR ERGOSTEROL SYNTHESIS.

CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 5-alpha-cholest-

8,24-dien-3-beta-ol -> S-adenosyl-L-homocysteine + 24-methylene-5-

alpha-cholest-8-en-3-beta-ol.

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DR EMBL; AF031941; AAC26626.1;

DR InterPro: IPR001601; Methyltransf.

DR InterPro: IPR000051; SAM_bind.

KW Sterol biosynthesis; Transferase; Methyltransferase.

SW SWOENCE 376 AA; 43085 MW; 369094aFCDDEDK0 CRC64;

Query Match 10.3%; Score 189; DB 1; Length 376;

Best Local Similarity 21.6%; Pred. No. 1.8e-08;

Matches 74; Conservative 55; Mismatches 133; Indels 80; Gaps 13;

QY 59 KDKKKLQKGIAE---FYDESSGLMENINGDHHNG-FYDSDS---TVSLSDHRAAOIR 110

DB 59 KDEDEKRLNDYSQLTHHYLVYDTDFEYEGWGSSFFHSRYKYGAEAFROATARHEHFLAHKM 118

QY 111 MIOESLRFASVSEERSKWPISYDVCGIGSSRYLAKKFGATSVGTLISVVOGRANAL 170

DB 119 NLNENMK-----VDVCGCGVGGPGEITRFDTCEIVGLANNNOYQIERANHY 164

QY 171 AAAAGLADKVSFOYADALQOPFSDGQFDLVWMSGEGHMPDKARFVGLARVAAPGATII 230

DB 165 AKKTHLDKLSYVKGDFMOMDFEPESFDAYVAIATVAHAPLDEGVSTIYVLAAPGIFG 224

QY 231 IVTWC-----HRDLG-----PDEOSLH--PWEODLLKICDA- 260

DB 225 VYEVMTDKYDETNEHRKIAVGLIEVDGIPKMSRKVAEQALKNVGEIIFYQDLADVD 284

QY 261 ----YLP-----AMCST--SDYVKLLQSLSLQDIKSEDSFVAPFPAVARSAPFTWGL 310

DB 285 DEIPWYPLSGDLKFCOTFGDYLTVFRTSRI-----GRFITTESVGLMEKI----- 330

QY 311 SSLLSGQKTKAL---APLMLEGYKKDLIKFAIITCRP 349

DB 331 -GLAPKSGKYTHALEDAVAALVLEVGGRQKLETFPMALVYVRP 371

RESULT 4

YLP3_PSEPU STANDARD; PRT; 394 AA.

AC P31049;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical 44.7 kDa protein in LpD-3.5 region (ORF3).

OS Pseudomonas putida.

OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;

OC Pseudomonas.

NCBI_TaxID=303;

RM [1]

RP SEQUENCE FROM N.A.

RC STRAIN=PPG2;

RA Lorenz D., Sokatch J.R.;

RL Submitted (MUG-1992) to the EMBL/GenBank/DBJ databases.

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CC

DR EMBL; X55704; CAA39234.1;

DR InterPro: IPR003333; CMAS.

DR InterPro: IPR001601; Methyltransf.

DR InterPro: IPR000051; SAM_bind.

KW Hypothetical protein.

SW SEQUENCE 394 AA; 44656 MW; 8CD61FE9495302AF CRC64;

Query Match 9.5%; Score 174; DB 1; Length 394;

Best Local Similarity 30.5%; Pred. No. 3.5e-07;

Matches 51; Conservative 30; Mismatches 58; Indels 28; Gaps 7;

QY 54 EOKPKK--DDKKLQKGIAEFYDESSGLMENINGDH-MHNG---FYDSSTVLSL----- 102

DB 90 EQPERSHDKRTAEALSYHYDVSNAYQ-LMDQDMAYSCAYREPNDNLDAQOQKF 148

QY 103 DHPAAQIMIOESLRFASVSEERSKWPISYDVCGIGSSRYLAKKFGATSVGTLSPV 162

DB 149 DHLCKRLNLNGDY-----LIDVCGCGMGGLAFARREYDAKVFGLTSKE 193

QY 163 QAQRANMLAAGLADKVSFOYADALQOPFSDGQFDLVWMSGEGHMPDKARFVGLARVAAPGATII 209

DB 194 QLKGRORVAKBGLTKVDYDQILDYRDL-ODGRFDKVVSYGMFEBV 239

RESULT 5

YE05_MYCTU

AC P71673; STANDARD; PRT; 274 AA.

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Hypothetical protein RY1405C precursor.

GN RY1405C OR MY1449 OR MYCY21BA.22C.

OS Mycobacterium tuberculosis.

OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;

OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.

NCBI_TaxID=1773;

RM [1]

RP SEQUENCE FROM N.A.

RC STRAIN=H37RV;

RX MEDLINE=98295987; PubMed=9634230;

RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,

RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,

RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

RA Davies R., Devlin K., Feltham T., Gentles S., Hamlin N., Holtroyd S.,

RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sultison J.E., Taylor K., Whitehead S., Barrell B.G.:
 RA "Deciphering the biology of Mycobacterium tuberculosis from the
 RA complete genome sequence.";
 RL Nature 393:537-544(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RA "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RA laboratory strains.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: STRONG, TO M.TUBERCULOSIS RV1403C AND SOME, TO
 CC R.SPAREOIDES PMTA.
 CC -----
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 CC -----
 CC EMBL: Z80108; CAB02184.1; -;
 DR EMBL: AE007016; AAK45714.1; -;
 DR TIGR: MT1449; -;
 DR TubercuList: RV1405C; -;
 DR InterPro: IPR000051; SAM_bind.
 KM Hypothetical protein; Signal; Complete proteome.
 FT SIGNAL 1 30
 FT CHAIN 31 274
 FT SEQUENCE 274 AA; 29262 MW; 3CF2932FE9E3531CA CRC64;
 SQ
 Query Match 8.5%; Score 156; DB 1; Length 274;
 Best Local Similarity 36.1%; Pred. NO. 7e-06;
 Matches 43; Conservative 16; Mismatches 56; Indels 4; Gaps 3;
 QY 132 IVDCGIGGSSRYLAKFGATSVGITLSPVOAQRANALAAAGLADVSFOVADALQOP 191
 Db 53 VLDVAAGSGNIS-LPAATGATVISTDTLPFLQSGRAAQQGTT-LQYQENAAQLP 109
 QY 192 FSDGQFDLWMSGEHMPDKAFVGLARVAAPGAIITVTW-CHRDLPDEQSLHPW 249
 Db 110 FADDEFPTVISAIGVFAPDQAAADLIVRCRPGGTIGVISWCEGFGHMLATIRPY 168
 RESULT 6
 CFA_ECOLI STANDARD; PRT; 381 AA.
 ID CFA_ECOLI
 AC P30010;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cyclopropane-fatty-acyl-phospholipid synthase (EC 2.1.1.79)
 DE (Cyclopropane fatty acid synthase) (CFA synthase).
 GN CFA OR CDF A OR B1661.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia
 OC NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A., SEQUENCE OF 1-8, AND CHARACTERIZATION.
 RC STRAIN-K12;
 RA MEDLINE-93075691; PubMed-1445840;
 RA Wang A.-Y., Grogan D.W., Cronan J.E. Jr.;
 RA "Cyclopropane fatty acid synthase of Escherichia coli: deduced amino
 RA acid sequence, purification, and studies of the enzyme active site.";

RL Biochemistry 31:11020-11028(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / RR28;
 RA Eberhardt S.M.R., Richter G., Gimbel W., Werner T., Bacher A.;
 RL Submitted (NOV-1992) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE-97426617; PubMed-9278503;
 RA Blatter F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Colloido-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.D.,
 RA Mau B., Shao Y.;
 RA "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE-97251357; PubMed-9097039;
 RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
 RA Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M.,
 RA Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,
 RA Motomura K., Nakade S., Nakamura Y., Nishimoto H., Nishio Y.,
 RA Oshima T., Saito N., Sempel G., Seki Y., Sivasubaram S.,
 RA Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,
 RA Yamamoto Y., Horinuchi T.;
 RA "A 570-kb DNA sequence of the Escherichia coli K-12 genome
 RA corresponding to the 28.0-40.1 min region on the linkage map.";
 RL DNA Res. 3:363-377(1996).
 CC -1- FUNCTION: TRANSFERS A METHYLENE GROUP FROM S-ADENOSYL-L-METHIONINE
 CC TO THE CIS DOUBLE BOND OF AN UNSATURATED FATTY ACID CHAIN
 CC RESULTING IN THE REPLACEMENT OF THE DOUBLE BOND WITH A METHYLENE
 CC BRIDGE.
 CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + phospholipid
 CC olefinic fatty acid -> S-adenosyl-L-homocysteine + phospholipid
 CC cyclopropane fatty acid.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -----
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 CC -----
 CC EMBL: M98330; AAA23562.1; -;
 DR EMBL: X69109; -; NOT_ANNOTATED_CDS.
 DR EMBL: AE000261; AAC74733.1; -;
 DR EMBL: D90809; BAA15428.1; -;
 DR EMBL: D90810; BAA15437.1; -;
 DR PIR: A44292; A44292;
 DR Ecogene; EG11531; Cfa.
 DR InterPro: IPR003333; CMA5.
 DR InterPro: IPR001601; Methyltransf.
 DR InterPro: IPR000051; SAM_bind.
 DR Pfam: PF02353; CMA5; 1
 KM Transferase; Methyltransferase; Lipid synthesis; Complete proteome.
 FT INIT_MET 0
 FT CONFLICT 1 1 S -> R (IN REF. 2).
 FT CONFLICT 7 7 E -> G (IN REF. 2).
 FT CONFLICT 24 24 S -> N (IN REF. 2).
 FT CONFLICT 38 38 I -> T (IN REF. 2).
 FT SEQUENCE 381 AA; 43777 MW; 1F07B220C7E08ADF CRC64;
 SQ
 Query Match 8.3%; Score 152; DB 1; Length 381;
 Best Local Similarity 24.1%; Pred. NO. 2.3e-05;
 Matches 61; Conservative 40; Mismatches 94; Indels 58; Gaps 12;
 QY 71 EFDSSGLMNINGDHHHG---FYDSSTVSLSDHRAQIRIQLSRRASVSEERSK 127
 Db 117 EHYDGLNDFSRMLDPFQWYSCAYWKAD---NLESQAQAKLMKICERLQD-----K 165


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UBIG_RALSO
ID UBIG_RALSO STANDARD; PRT; 238 AA.
AC 08Y025;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 3-demethylubiquinone-9-3-methyltransferase (EC 2.1.1.64) (3,4-
DE dihydroxy-5-hexaprenylbenzoate methyltransferase) (DHNB
DE methyltransferase).
GN UBIG OR RSC0898 OR RS04517.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Catolico L.,
RA Chandler M., Choise N., Claudel-Renard C., Cunac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
RA Signier P., Thiebaut P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
CC -1- CARBOLYTIC ACTIVITY: S-adenosyl-L-methionine + 3-
CC -1- demethylubiquinone-9 = S-adenosyl-L-homocysteine + ubiquinone-9.
CC -1- PATHWAY: Ubiquinone biosynthesis.
CC -1- SIMILARITY: BELONGS TO THE UBIG/COQ3 FAMILY.
CC -----
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CC -----
CC EMBL: AL646061; CAD14600.1; ALT. INT.
CC InterPro: IPR001601; Methyltransf.
CC InterPro: IPR000051; SAM_bind.
CC InterPro: IPR004033; UblE/COQ5_Metrif.
CC Pfam: PF01209; UblE_methyltran; 1.
CC Ubiquinone biosynthesis; Transferase; Methyltransferase;
CC Complete proteome.
CC KW
CC SO SEQUENCE 238 AA; 25894 MW; 18114F00BF315808 CRC64;

Query Match 7.5%; Score 137; DB 1; Length 238;
Best Local Similarity 28.6%; Pred. No. 0.00023;
Matches 57; Conservative 26; Mismatches 82; Indels 34; Gaps 8;
OY 90 HGYDSDSTVS-LSDRRAQIRMIQESLRFASVSEERSKPKSIIVGCGIGSSRYLAK 148
DB 21 HRWMDNSEKRPLEINPLRDMWISTAPLAG-----KRVVDGCGGGLSSSMAR 71
OY 149 KEGATSVGTTLSFVQARANALAAQGLADKVSFOVADAL--COQPSDGFDLVMSWESG 206
DB 72 A-GANVKGIDLSRKALRVDLHSLRAGVAVDYDEIAEAALANEP---GSFVVTCTEML 127
OY 207 EHMFDKAKFYGELARVAARPAIIITWCHRDGPRDQSLHPEQDLKKTCAYI----- 262
DB 128 EHVDPDASVVRACATLVKPGGHVFST-----IHRNAKAYLLAVIAEYVLNM 175
OY 263 LPAMCSTDYVKLLQSLSL 281
DB 176 LPR--GTHDYAKIRPSEL 192

RESULT 10
UBIG_PASMU
ID UBIG_PASMU STANDARD; PRT; 242 AA.
AC 09CM16;

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DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 3-demethylubiquinone-9-3-methyltransferase (EC 2.1.1.64) (3,4-
DE dihydroxy-5-hexaprenylbenzoate methyltransferase) (DHNB
DE methyltransferase).
GN UBIG OR PM0840.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Pm70;
RX MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang O., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC -1- CARBOLYTIC ACTIVITY: S-adenosyl-L-methionine + 3-
CC -1- demethylubiquinone-9 = S-adenosyl-L-homocysteine + ubiquinone-9.
CC -1- PATHWAY: Ubiquinone biosynthesis.
CC -1- SIMILARITY: BELONGS TO THE UBIG/COQ3 FAMILY.
CC -----
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CC -----
CC EMBL: AE006122; AK02924.1; -
CC InterPro: IPR001601; Methyltransf.
CC InterPro: IPR000051; SAM_bind.
CC Ubiquinone biosynthesis; Transferase; Methyltransferase;
CC Complete proteome.
CC KW
CC SO SEQUENCE 242 AA; 27284 MW; B6318FA1ACC01BDD CRC64;

Query Match 7.3%; Score 134.5; DB 1; Length 242;
Best Local Similarity 24.9%; Pred. No. 0.00038;
Matches 52; Conservative 37; Mismatches 75; Indels 45; Gaps 11;
OY 116 LPFASVSEERSKMP-KSIYDVCGGIGSSRYLAKKFGATSVGTTLS--PVQARANALAA 172
DB 35 LRLSYIAAQANGLTGKRVLDVCGGGLSBSNAKQ-GAITYTGIDMSAPLQVARKHALPS 93
OY 173 AGCL-ADKVSFOVADALQOPFS-----DGOVDLYMSWESGSHMDKAKFYGELARVAA 224
DB 94 --GLHIDYQOITTEFLQNOTALFAERGEDKDVITCMELEHVPDPSSIAACKQQLK 151
OY 225 PGAIITIVTWCHRDLPDPDEQSLHPW-----EODLLKKI-----CDAYILPA---WCS 268
DB 152 PNCVIEFST-----INRTLKAMALVIIGAYVLKMLPKRGTHDYDKFKIRPELLHMKD 203
OY 269 TSDYVKLLQSLSLQDIKSEDSWRFVAPFW 297
DB 204 EA-----QLTCLDMVGYHYNPLTGKFW 225

RESULT 11
UBIG_NEIMB
ID UBIG_NEIMB STANDARD; PRT; 238 AA.
AC 09JX17;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 3-demethylubiquinone-9-3-methyltransferase (EC 2.1.1.64) (3,4-
DE dihydroxy-5-hexaprenylbenzoate methyltransferase) (DHNB
DE methyltransferase).
GN UBIG OR NMB2030.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;

```

[1]
 RN SEQUENCE FROM N.A.
 RP STRAIN-MC58 / Serogroup B;
 RC MEDLINE=20175755; PubMed-10710307;
 RA Tettein H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
 RA Elsen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
 RA Nelson W.C., Gwin M.L., DeBoy R., Peterson J.D., Hickey E.K.,
 RA Hafiz D., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
 RA Mason T., Clecko A., Parksey D.S., Blair E., Clifton H., Clark E.B.,
 RA Cotton M.D., Uterback T.R., Khouri H., Qin H., Vamathevan J.,
 RA Gill J., Scarlato V., Maignan V., Pizzo M., Grandi G., Sun L.,
 RA Smith H.O., Fraser C.M., Moxon E.R., Rappelli R., Venter J.C.;
 RT *Complete genome sequence of *Neisseria meningitidis* serogroup B strain
 MC58.
 RL Science 287:1809-1815(2000).
 CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3-
 CC demethylubiquinone-9 -> S-adenosyl-L-homocysteine + ubiquinone-9.
 CC -1- PATHWAY: Ubiquinone biosynthesis.
 CC -1- SIMILARITY: BELONGS TO THE UBIG/COQ3 FAMILY.
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 CC -----
 CC DR EMBL: AE002552; AAF42352.1; ALT_INIT.
 DR TIGR: NMB2030;
 DR InterPro: IPR001601; Methyltransf.
 DR InterPro: IPR000051; SAM_bind.
 KM Ubiquinone biosynthesis; Transferase; Methyltransferase;
 KM Complete proteome.
 SQ SEQUENCE 238 AA; 26529 MW; 7CA7305A824BADFE CRC64;

Query Match 7.2%; Score 131.5; DB 1; Length 238;
 Best Local Similarity 27.1%; Pred. No. 0.00066;
 Matches 46; Conservative 25; Mismatches 64; Indels 35; Gaps 6;

QY 130 KSIIVVGGIGGSSRYLAKFGATSVGTLSPVOAORANALAAOGLADKVSFO---VAD 186
 DB 53 KAVLDVGGCGGILAESMARGAFAVKGIDMAQSELTALHAAIINNVD-IEECIRVAD 111
 QY 187 -ALQPFSDGDFDLVSMESGEHMDPKAFVGEIARVAAPGAIITVTWCHRDLPDEOS 245
 DB 112 LAEAPHS---EDVYTCMEHMEHVDPALIVACANLVKPDGVFEST----- 156
 QY 246 LHPWODLLKRICDAYILPANCSTSDYVKLLQSLSDIKSEDSWRFVAP 295
 DB 157 INKNPKSYLHLIVAAEYL-----LKEVPKGTIDMKKFIAP 191

RESULT 12
 UBIG_RICCN
 ID UBIG_RICCN STANDARD: PRT: 289 AA.
 AC Q92H07;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 3-demethylubiquinone-9-3-methyltransferase (EC 2.1.1.64) (3,4-
 DE dihydroxy-5-hexaprenylbenzoate methyltransferase) (DHMB
 DE methyltransferase).
 GN UBIG OR RC0965.
 OS Rickettsia conorii.
 CC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 CC Rickettsiaceae; Rickettsiase; Rickettsia.
 OX NCBI_TaxID=781;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Malish 7;
 RX MEDLINE=21442074; PubMed=11557893;
 RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,

RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
 RA Raoult D.;
 RT "Mechanisms of evolution in *Rickettsia conorii* and *R. prowazekii*.";
 RL Science 293:2093-2098(2001).
 CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3-
 CC demethylubiquinone-9 -> S-adenosyl-L-homocysteine + ubiquinone-9.
 CC -1- PATHWAY: Ubiquinone biosynthesis.
 CC -1- SIMILARITY: BELONGS TO THE UBIG/COQ3 FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 RPEL INSERT DOMAIN.
 CC -----
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 CC -----
 CC DR EMBL: AE008649; AAL03503.1;
 DR InterPro: IPR001601; Methyltransf.
 DR InterPro: IPR000051; SAM_bind.
 DR TIGRFAMS: TIGR01045; RPE: 1.
 KM Ubiquinone biosynthesis; Transferase; Methyltransferase;
 KM Complete proteome.
 FT DOMAIN 50 RPEL INSERT.
 SQ SEQUENCE 289 AA; 33074 MW; 4CAEA6827EC7B977 CRC64;

Query Match 7.2%; Score 131.5; DB 1; Length 289;
 Best Local Similarity 22.5%; Pred. No. 0.00085;
 Matches 60; Conservative 51; Mismatches 91; Indels 65; Gaps 12

QY 61 DKKKLQKGAIEFYDESSGLMENWGDH-----MHGCFYDSST--- 98
 DB 5 DKKELEK-----FEKISHMWMKDGEGILHRINPIRLEYLIEKITTHYRHLKLYRE 59
 QY 99 -VSLSDHRAQIRMIQE-----SLRFASVSEBSKMPKSIYDVGCGIG--S 142
 DB 60 ELVGMNQHSTAYALVAREPASSRLTKRLPLEAEFEKMSNDISK--LEILDVCGG-GGLIA 116
 QY 143 SHYLAKEFGATSVGTLSPVOAORANALAAOGLADKVSFOVDALQPFSDGDFLWMS 202
 DB 117 TPLAAGFVNTALDQSNIEF--ATAVAKENV--KINK-LOSTIEELSDKLYDVIC 171
 QY 203 MESGEHMDPKAFVGEIARVAAPGAIITVTWCHRDLPDEOSLHPWODLLKRICDAY 262
 DB 172 LEVIEHVENVOGFIINLVKIRPNGMALIST-----INTRKAYILGIIVAEY 219
 QY 263 LPANC--STSDYVKLLQSLSDIKSE 287
 DB 220 ILGWPKNTHDYSKFLKPLEIYEMLTD 246

RESULT 13
 YE03_MYCTU
 ID YE03_MYCTU STANDARD: PRT: 274 AA.
 AC P71671;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein Rv1403c precursor.
 GN Rv1403C OR M71447 OR MYC721B4.20C.
 OS Mycobacterium tuberculosis.
 CC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
 CC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holtroyd S.,

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RA MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagers K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Raitandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrall B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis Z2491."
RT Nature 404:502-506(2000).
CC -I- CATALYTIC ACTIVITY: S'-adenosyl-L-methionine + 3-
CC demethylubiquinone-9 - S'-adenosyl-L-homocysteine + ubiquinone-9.
CC -I- PATHWAY: Ubiquinone biosynthesis.
CC -I- SIMILARITY: BELONGS TO THE UBIG/COO3 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC -----
CC CC EMBL; AL162753; CAB83709.1; -
CC DR InterPro: IPR001601; Methyltransf.
CC DR InterPro: IPR000051; SAM bind.
CC KW Ubiquinone biosynthesis; Transferase; Methyltransferase;
CC Complete proteome.
SO SEQUENCE 238 AA; 26571 MW; 629DF6EFD23BA8AA CRC64;

Query Match 7.1%; Score 129.5; DB 1; Length 238;
Best Local Similarity 26.5%; Pred. No. 0.00097;
Matches 45; Conservative 26; Mismatches 64; Indels 35; Gaps 6;

QY 130 KSIYVVGCGIGSSRYLAKKFGATVGTITLSPVQAQRNALAAAGLADKKSFG---YAD 186
DB 53 KRLVDVGGGGGGLIASSMRGAAFYKGIIDMAQSLETRALRLHALNVAAD-TEYECIRVED 111
QY 187 -ALADQPFSDGQFDILVWSNESGEHMPDKAKFYGEIARVAAPAIITIIYVWCHRDLGPDDEOS 245
DB 112 LAEAPPHS---FDVYVTCNEMHEHVPDPAIYIRACAKLVKPDGMVFESF----- 156
QY 246 LHPWQDILKIKICQAYIYIPAMCSISDYKKLLQSLSLQDIKSEDSRFPAP 295
DB 157 INKNRXYLHLIVAAYL-----LKFVKGTRDMKKFIVP 191

RESULT 15
UBIG_PSEAE
ID UBIG_PSEAE STANDARD; PRT; 232 AA.
AC Q9H263;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 3-demethylubiquinone-9 3-methyltransferase (EC 2.1.1.64) (3,4-
DE dihydroxy-5-thexaprenylbenzoate methyltransferase) (DHNB
DE methyltransferase).
DE UBIG OR PA3171.
OS Pseudomonas aeruginosa.
OC Bacteriia; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
[1]
RA SEQUENCE FROM N.A. A.
RA STRAIN=ATCC 15692 / PAOI;
RA MEDLINE=20437337; PubMed=10984043;
RA Hickey M.J., Brinkman F.S.L., Hufnagle M.O., Kowalik D.J., Lagrou M.,
RA Gader R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RA "Complete genome sequence of Pseudomonas aeruginosa PAOI, an
RT
```

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RT opportunistic pathogen."
RL Nature 406:959-964(2000).
CC -1- CATALYTIC ACTIVITY: S'-adenosyl-L-methionine + 3-
CC demethylubiquinone-9 = S'-adenosyl-L-homocysteine + ubiquinone-9.
CC -1- PATHWAY: Ubiquinone biosynthesis.
CC -1- SIMILARITY: BELONGS TO THE UBIQ/COQ3 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AE004741; AAC06559.1; -.
DR InterPro: IPR001601; Methyltransf.
DR InterPro: IPR000051; SAM_bind.
DR InterPro: IPR004033; UbiE/COQ5_Metrf.
DR Pfam: PF01209; UbiE_methyltran; 1.
KW Ubiquinone biosynthesis; Transferase; Methyltransferase;
KW Complete proteome.
SQ SEQUENCE 232 AA; 25859 MW; 6A3EA81D90A4177C CRC64;

Query Match 7.0%; Score 128; DB 1; Length 232;
Best Local Similarity 29.18; Pred. No. 0.0013;
Matches 43; Conservative 27; Mismatches 60; Indels 18; Gaps 7;

OY 90 HGEYDSSTVS-LSDHRAQIREMIOESLRPASVSERSKWPMSIYDVGCGIGSSRYLAK 148
DB 17 HRWMDRESEFKPLNDINPLRYWIMIDERAGLAG-----KKVIDIGCGGGILSEAMNQ 67

OY 149 KEGATVSGITL--SPVQAQRANALAAOGLADKVSFOVADALQOPFS--DGQFDLVMSMS 205
DB 68 R-GASVTCIDMGEPALVARRHQLES--GVA--VDYRQITAEQMAEMRPGQFDVYTCLEM 122

OY 206 GEHMPDKAKFVGEIARVAPGAIITITVT 233
DB 123 LEHVPDPASVIRACHRLVPGGQVPLST 150

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Search completed: March 18, 2003, 17:38:08
 Job time : 14 secs

Df 150 DVGCGIGSSRYLAKKYGAKLSRLATITLSPVOQAQBAQOALDAQGLNGKVSEFEVDALNQP 209

OY 192 FSDGDFOLWMSWESEHHPDPAKFPELGELARVAAPCAIIITYTCWRDUGDPBDSCHPMEQ 251
+:::|||||++++|||++|||+|||||+|||||+|||+
Db PPEGFDFLWMSWESEHHPDKKKFYNEVLVRAAPAAGRIIIVYWCRRDLSPESESLROBEK 269

OY 252 DLKKICGAYVLPACSTSDYVKLLQSILDIODIKSEDSRFVAPWPVIRSAFPWKGS 311
|||+|||+|||||+|||||+|||||+|||||+|||||+|||||+|||||+|||||+|||||+
Db DILNKICGAYVLPACSTADYVKLLDLSMEDIKSADSNDHVAPWPVIRSAFPWKGIT 329

OY 312 SLUSSGORTINGCALAMPMTIEGYKKDLIKFAITTCRK 349
|||+|||+|||||+|||||+|||||+|||||+|||||+|||||+|||||+|||||+|||||+
Db SLNRSGWKTINGAMVMPMTIEGYKKGVYKFAITTCRKP 367

RESULT 2

Q9XIP9 PRELIMINARY; PRT; 348 AA.

Ac Q9XIP9
Dt 01-NOV-1999 (TREMBLrel. 12. Created)
Dt 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
Dt 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
De Gamma-tocopherol methyltransferase (Atlg64970/F13011_27).
GN F13011.27.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OX eurosids II; Brassicales; Brassicaceae; Arabidopsits.
NCBI_TaxID=3702;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=CV. COLUMBIA;
RA Federpiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA Alfai H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,
RA Gonzalez A., Kremenetskaia I., Kim C., Ienz C., Li J., Liu S.,
RA Lyons S., Schwartz J., Shinn P., Tortum M., Vysotskaia V.S.,
RA Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
[12]
RN SEQUENCE FROM N.A.
RP Cheuk R., Chen H., Kim C.J., Koeseema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jiang P.X., Jones T., Kamlya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Tortum M., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis cDNA clones."
RL Submitted (Jul-2001) to the EMBL/GenBank/DBJ databases.
[13]
RN SEQUENCE FROM N.A.
RP Kim C.J., Chen H., Cheuk R., Meyers M.C., Shinn P., Banh J.,
RA Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jones T., Kamlya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Seki M., Southwick A., Tang C.C., Tortum M., Wu H.C., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis ORF clones."
RL Submitted (Mar-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC006193; AACD38271.2; -
DR EMBL: AY049258; AAK83600.1; -
DR EMBL: AY090280; AAL90941.1; -
DR InterPro: IPR001601; Methyltransf.
KW InterPro: IPR000051; SAM_bind.
NW Methyltransferase; Transferase.
SO SEQUENCE 348 AA; 38075 MW; E9290758C2E83B73 CRC64;

Query Match 63.1%; Score 1154.5; DB 10; Length 348;
Best Local Similarity 69.4%; Pred. No. 1e-86;
Matches 227; Conservative 28; Mismatches 61; Indels 11; Gaps 4;

| | | | |
|-----------------------------------------------------------------|-----------------------------------------------------------------------|----------------------------------------------------------------|--------------|
| Oy | 32 | GPBSWAPIRASASAE-----RCGIVTEQPKKDKKDKKLGIAEFYDESSGLMENTWG | 85 |
| | 1 | : : : : | 11 |
| | 23 | GSKSLLRRSPSSSSVSMTTTRGNVAVAANAATSTEE--ALKRGIAEFNETSGLMBEETWG | 80 |
| Oy | 86 | DHMHGFGYDSSTVSLSD--HRAAOIRMIQESLRFASVS--EERSKMPKSIYDVCGGIGGS | 142 |
| | 81 | DHMHGFGYDPPSSVGLSDSGHKEAQIRMIESTLRFAGVTDEEBEKKIKKVVYDVGCGIGGS | 140 |
| Oy | 143 | SRYLAKKRGAGTSVGTTLSPVOAQRNALAAAGLADKYSFOYADALDQPFSDGQPDLYWS | 202 |
| | 141 | SRYLASKGAGCIGITTLSPVOAKRANDLAAAOSSLAKHKSFOYADALDQPFEDGKFDLYWS | 200 |
| Oy | 203 | MESGHEMPDKAKFVVELARVAAPGALIIIVTWCCHRDLPDEQSLHPMEQDILKTKCDAYY | 262 |
| | 201 | MESGHEMPDKAKFVVELARVAAPGCRRIIIVTWCCHRNLSGEBALDQPMQNIIDKTKCRFFY | 260 |
| Oy | 263 | LPAMCSTDYVKLLQSLSLQDIKSEDSWRFVAFMPPAVIRSAFTWKGLSLLSGQKTIK | 322 |
| | 261 | LPAMCSTDYVNLQSLSDIKCADWSENNVAFMPPAVIRFALTKGLVSLRSGMKSIK | 320 |
| Oy | 323 | GALAMPIMEGKYKDLIRFAITTCRP | 349 |
| | 321 | GALTPMLMIEGKYKGVIRKFIITCCKP | 347 |
| RESULT 3 | | | |
| O9ZSKI | 1D | PRELIMINARY; | PRT; 348 AA. |
| AC | O9ZSKI; | | |
| PT | 01-MAY-1999 (TREMBUREL 10, Created) | | |
| PT | 01-MAY-1999 (TREMBUREL 10, Last sequence update) | | |
| PT | 01-MAR-2002 (TREMBUREL 20, Last annotation update) | | |
| DE | Gamma-tocopherol methyltransferase. | | |
| GN | G-TMT. | | |
| OS | Arabidopsis thaliana (Mouse-ear cress). | | |
| OC | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; | | |
| OC | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; | | |
| CC | eucosids II: Brassicales; Brassicaceae; Arabidopsis. | | |
| OX | NCBI_Taxid:3702; | | |
| RN | (1) | | |
| RP | SEQUENCE FROM N.A. | | |
| RA | Shintani D.K., Dellapenna D.; | | |
| RT | "Elevating Vitamin E content of plants through metabolic | | |
| RT | engineering"; | | |
| RL | Science 0:0-0(1998) | | |
| DR | EMBL; AF104220; AAD02882.1; - | | |
| DR | InterPro: IPR001601; Methyltransf. | | |
| DR | InterPro: IPR000051; SAM bind. | | |
| KW | Methyltransferase; Transferase. | | |
| SO | SEQUENCE 348 AA; 38091 MW; 44DB18A722E0725F CRC64; | | |
| Query Match 62.9%; Score 1151.5; DB 10; Length 348; | | | |
| Best Local Similarity 69.1%; Pred. No. 1.8e-86; | | | |
| Matches 226; Conservative 29; Mismatches 61; Indels 11; Gaps 4; | | | |
| Oy | 32 | GPBSWAPIRASASAE-----RCGIVTEQPKKDKKDKKLGIAEFYDESSGLMENTWG | 85 |
| | 1 | : : : : | 11 |
| | 23 | GSKSLLRRSPSSSSVSMTTTRGNVAVAANAATSTEE--ALKRGIAEFNETSGLMBEETWG | 80 |
| Oy | 86 | DHMHGFGYDSSTVSLSD--HRAAOIRMIQESLRFASVS--EERSKMPKSIYDVCGGIGGS | 142 |
| | 81 | DHMHGFGYDPPSSVGLSDSGHKEAQIRMIESTLRFAGVTDEEBEKKIKKVVYDVGCGIGGS | 140 |
| Oy | 143 | SRYLAKKRGAGTSVGTTLSPVOAQRNALAAAGLADKYSFOYADALDQPFSDGQPDLYWS | 202 |
| | 141 | SRYLASKGAGCIGITTLSPVOAKRANDLAAAOSSLAKHKSFOYADALDQPFEDGKFDLYWS | 200 |
| Oy | 203 | MESGHEMPDKAKFVVELARVAAPGALIIIVTWCCHRDLPDEQSLHPMEQDILKTKCDAYY | 262 |
| | 201 | MESGHEMPDKAKFVVELARVAAPGCRRIIIVTWCCHRNLSGEBALDQPMQNIIDKTKCRFFY | 260 |
| Oy | 263 | LPAMCSTDYVKLLQSLSLQDIKSEDSWRFVAFMPPAVIRSAFTWKGLSLLSGQKTIK | 322 |
| | 261 | LPAMCSTDYVNLQSLSDIKCADWSENNVAFMPPAVIRFALTKGLVSLRSGMKSIK | 320 |
| Oy | 323 | GALAMPIMEGKYKDLIRFAITTCRP | 349 |
| | 321 | GALTPMLMIEGKYKGVIRKFIITCCKP | 347 |

DB 261 LAMCTSDYVNLQSHSLQDICKADMSVNAFPAVIRALTATWGLVSLRSKSTIK 320
 OY 323 GALAMPLEMGYKKDLKFAITTCRKP 349
 DB 321 GALTPLMIEGKGVKGVITTCOKP 347

RESULT 4

OBYW13 PRELIMINARY: PRT: 280 AA.
 AC 08YW13: 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Gamma-tocopherol methyltransferase.
 GN ALR1803.
 OS Anabaena sp. (strain PCC 7120).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
 OX NCBI_TaxID=103690.
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21595285; PubMed=11759840;
 RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
 RA Matanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
 RA Yasuda M., Tabata S.:
 RT *Complete genomic sequence of the filamentous nitrogen-fixing
 RT cyanobacterium Anabaena sp. strain PCC 7120.*;
 RL DNA Res. 8:205-213(2001).
 DR EMBL: AP003587; BAB73502.1;
 DR InterPro: IPR001601; Methyltransf.
 DR InterPro: IPR000051; SAM_bind.
 DR Pfam: PF01209; Ublc_methyltran; 1.
 KW Transferrase; Methyltransferase; Complete proteome.
 SQ SEQUENCE 280 AA; 31309 MW; 663FD841294B9133 CRC64;

Query Match

Best Local Similarity 36.0%; Score 659; DB 16; Length 280;
 Matches 138; Conservative 42; Mismatches 92; Indels 8; Gaps 3;

OY 65 LKGIAPFYDESSGLMWNMGDMHGFYDSSTVSLSDHRAQIRIQTOSLAPASVSE 124
 DB 5 LVQOIOQFYDASSGLWEEIEMHGHGYGADGT-EQKNRQAOIDILELWAGV-- 60
 OY 125 RSKWPKSIYVYGGIGSSRYLAKKFGATSVGTLSPVQARANALAAOGLADKVSFOY 184
 DB 61 --QTAENILDYGGIGSSRYLAKKFGATSVGTLSPVQARANALAAOGLADKVSFOY 118
 OY 185 ADALQOPEFSDGQFDLVWMSMESGEMPDRAKFGVGLARVAAGALIIITVWCHRDLPDEQ 244
 DB 119 ANQAMPFDDNSFDLVWMSLESSEGMHPDKTKFLOECYRVLRPGKLIWVWCCHRP--TDKT 176
 OY 245 SLHPWEDDLKKICDAIYLPAMCSTSDYVNLQSHSLQDICKADMSVNAFPAVIRSA 304
 DB 177 PLTADERKHLIEDIYRYVCLPYPVSLPVEYLAIRQLPLNNRTADMSVNAFPAVIRSA 236
 OY 305 FTWKGLSSLSGCKTKTGALAMPLEMGYKKDLKFAITTCRKP 344
 DB 237 FTTPQATFGLRACGTTTQALSLGALMRGTERGLIRFGL 276

RESULT 5

O55809 PRELIMINARY: PRT: 317 AA.
 AC 055809: 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE DELTA(24)-sterol C-methyltransferase.
 GN ERG6 OR SLR0089.

OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TaxID=1148;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96127529; PubMed=8590279;
 RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
 RA Sugitani M., Tabata S.:
 RT *Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
 RT region from map positions 64% to 92% of the genome.*;
 RL DNA Res. 2:153-166(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hiroseawa M., Sugitani M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
 RA Shimpo S., Takeuchi C., Wada T., Matanabe A., Yamada M., Yasuda M.,
 RA Tabata S.:
 RT *Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.*;
 RL DNA Res. 3:109-136(1996).
 DR EMBL: D64004; BAA10562.1;
 DR InterPro: IPR001601; Methyltransf.
 DR InterPro: IPR000051; SAM_bind.
 KW Transferrase; Methyltransferase; Complete proteome.
 SQ SEQUENCE 317 AA; 35571 MW; 98DD01C081B89F72 CRC64;

Query Match

Best Local Similarity 35.4%; Score 647.5; DB 16; Length 317;
 Matches 135; Conservative 45; Mismatches 102; Indels 3; Gaps 3;

OY 65 LKGIAPFYDESSGLMWNMGDMHGFYDSSTVSLSDHRAQIRIQTOSLAPASVSE 124
 DB 34 LYKRIKFFYDSSGLWEDVMEHGHGYGPHGYRI-DRROAOIDILELWAGV-- 91
 OY 125 RSKWPKSIYVYGGIGSSRYLAKKFGATSVGTLSPVQARANALAAOGLADKVSFOY 184
 DB 92 SAR-PKRIIDLGCGIGSSRYLAKKFGATSVGTLSPVQARANALAAOGLADKVSFOY 150
 OY 185 ADALQOPEFSDGQFDLVWMSMESGEMPDRAKFGVGLARVAAGALIIITVWCHRDLPDEQ 244
 DB 151 ANADLPFASDFPWSLESSEGMHPDKRAQVLOAMRKGLKGLIATWCHRPDPNG 210
 OY 245 SLHPWEDDLKKICDAIYLPAMCSTSDYVNLQSHSLQDICKADMSVNAFPAVIRSA 304
 DB 211 PLTADERKHLIEDIYRYVCLPYPVSLPVEYLAIRCGFGEIKRTADMSVNAFPAVIRSA 270
 OY 305 FTWKGLSSLSGCKTKTGALAMPLEMGYKKDLKFAITTCRKP 349
 DB 271 FDRPVLMALGOAGPKIINALCLRLMKYRGVGLRFGLLGIRP 315

RESULT 6

O8YV60 PRELIMINARY: PRT: 330 AA.
 AC 08YV60: 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Hypothetical protein A112121.
 GN A112121.
 OS Anabaena sp. (strain PCC 7120).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
 OX NCBI_TaxID=103690.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21595285; PubMed=11759840;
 RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
 RA Matanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,

*Biosynthesis of the ansamycin antibiotic rifamycin: deductions from

RT "Biosynthesis of the ansamycin antibiotic rifamycin: deductions from
RT the molecular analysis of the rif biosynthetic gene cluster of
RT *Amycolatopsis mediterranei* 5699.";
RL Chem. Biol. 5:69-79(1998).
RN [2]
RP SEQUENCE FROM N.A.
RP STRAIN=5699;
RC MEDLINE=98165773; PubMed=9497318;
RX Kim C.-G., Yu T.-W., Fryhle C.B., Handa S., Floss H.G.;
RA 3-Amino-5-hydroxybenzoic acid synthase, the terminal enzyme in the
RT formation of the precursor of mC7N units in rifamycin and related
RT antibiotics.";
RN J. Biol. Chem. 273:6030-6040(1998).
RL [3]
RN SEQUENCE FROM N.A.
RP STRAIN=5699;
RC MEDLINE=21201076; PubMed=11278540;
RX Yu T.-W., Mueller R., Mueller M., Zhang X., Draeger G., Kim C.-G.,
RA Leister E., Floss H.G.;
RA "Mutational analysis and reconstituted expression of the biosynthetic
RT genes involved in the formation of 3-amino-5-hydroxybenzoic acid, the
RT starter unit of rifamycin biosynthesis in *Amycolatopsis mediterranei*
RT 5699.";
RN J. Biol. Chem. 276:12546-12555(2001).
RL [4]
RN SEQUENCE FROM N.A.
RP STRAIN=5699;
RC August P.R., Tang L., Yoon Y.J., Ning S., Mueller R., Hutchinson C.R.

Submitted

RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF040570; AAC01738.1; -;
 DR InterPro; IPR001601; Methyltransf

KW Transfer:

KW Transferrase. 30295 MW; 4E65895C5A3BF1FC CRC64;
S0 SEQUENCE 272 AA; 30295 MW; 4E65895C5A3BF1FC CRC64;

Best Local :

Best Local Similarity 25.0%; Pred. No. 9.2e-15;
Matches 72; Conservative 64; Mismatches 122; Indels 30; Gaps 6

| | 1970 | 1980 | 1990 | 2000 |
|----|------|------|------|------|
| .. | - | - | - | - |

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9 IGGYDAFADLLDFOFGENLHHGWDEDSATLEETRLTDLRAGMLPL----- 57
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18
19
20

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      :|:|:| | | | | | | | | | | |
    58 ----RACRLDIGCGNGEPAIRMATANDYMTGISISEKOVERANDRAIKADYDDRVF 113

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$$\frac{1}{\sqrt{2}} \begin{pmatrix} 1 & 1 \\ 1 & -1 \end{pmatrix} \begin{pmatrix} \cos \theta & \sin \theta \\ -\sin \theta & \cos \theta \end{pmatrix} \frac{1}{\sqrt{2}} \begin{pmatrix} 1 & 1 \\ 1 & -1 \end{pmatrix}$$
[illegible]

QY 243 E923

Db 171 PAGELEA-DARVREVKGK--VVAAVSLDEQAHLREAGLEPESAEVDVSQYTRPSW---TK 224

QY 303 SAE :1

QY 303 SARTWAGDSUUSGVALNORLANE LRLICINACANLHALLICNE 268
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 225 AAEFEGLEGOALOHTEAAOFVTLGRFRASFSEEPSIGVLLTARPD 272

RESULT 11

RESULT 11
O9EY12
ID 00EY13
PRELIMINARY.
PRT: 278 AA.

AC Q9EYI2;
DT 01-MAR-2

| | | |
|----|-------------|-----------------------------------------|
| AC | 09EY12; | |
| DT | 01-MAR-2001 | (TREMblrel. 16, Created) |
| DT | 01-MAR-2001 | (TREMblrel. 16, Last sequence update) |
| DT | 01-MAR-2002 | (TREMblrel. 21, Last annotation update) |

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|----|----------|
| DT | 01-JUN-2 |
| DT | 01-MAR-2 |

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|----|-------------|-----------------------------------------|
| UT | 01-MAR-2001 | (11EMBLrel. 10, last sequence update) |
| DT | 01-JUN-2002 | (11EMBLrel. 21, last annotation update) |
| DE | SNOCM. | |
| GN | SNOCM | |

05 Streptococcus

US Streptomyces nogatalei; Actinobacteridae;
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteriales;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

